

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: Innogenetics sa.
- (B) STREET: Industriepark Zwijnaarde 7, box 4
- (C) CITY: Ghent
- (E) COUNTRY: Belgium
- (F) POSTAL CODE (ZIP): B-9052
- (G) TELEPHONE: 00 32 9 241 07 11
- (H) TELEFAX: 00 32 9 241 07 99

(ii) TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.

(iii) NUMBER OF SEQUENCES: 270

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: BR34-4-20

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG  
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
1 5 10 15

48

GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC  
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

96



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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTC	ACG	GAA	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTC	AAC	AGC	AAG	GGG	48
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1			5						10					15		
GCC	CAG	TGT	GGT	TAT	CGC	CGC	TGC	CGT	GCC	AGT	GGA	GTT	CTG	CCT	ACC	96
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
		20					25					30				
AGC	TTC	GGC	AAC	ACA	ATC	ACT	TGC	TAC	ATC	AAG	GCC	ACA	GCG	GCT	GCA	144
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
		35					40					45				
AGG	GCC	GCA	GGC	CTC	CGG	AAC	CCG	GAC	TTT	CTT	GTC	TGC	GGA	GAT	GAT	192
Arg	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
	50					55					60					
CTG	GTC	GTG	GTG	GCT	GAG	AGT										213
Leu	Val	Val	Val	Ala	Glu	Ser										
65					70											

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10					15		
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
		20					25					30				
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
		35					40				45					
Arg	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
	50					55					60					
Leu	Val	Val	Val	Ala	Glu	Ser										
65					70											

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-23-18

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAG GGG	48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC	96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA	144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT	192
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
CTG GTC GTG GTG GCT GAG AGT	213
Leu Val Val Val Ala Glu Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	



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PCT/EP94/01323

99

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-23-20

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTC	ACG	GAG	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTT	AAC	AGC	AAA	GGG	43
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10						15	
GCC	CAG	TGT	GGT	TAT	CGC	CGT	TGC	CGT	GCC	AGT	GGA	GTT	CTG	CCT	ACC	95
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
			20					25					30			
AGC	TTC	GGC	AAC	ACA	ATC	ACT	TGT	TAC	ATC	AAA	GCC	ACA	GCG	GCC	GCA	144
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
			35				40					45				
AAA	GCC	GCA	GGC	CTC	CGG	AGC	CCG	GAC	TTT	CTT	GTC	TGC	GGA	GAT	GAT	192
Lys	Ala	Ala	Gly	Leu	Arg	Ser	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
			50				55					60				
CTG	GTC	GTG	GTG	GCT	GAG	AGT										213
Leu	Val	Val	Val	Ala	Glu	Ser										
65					70											

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1           5           10           15
Ala Glu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
          20           25           30
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
          35           40           45
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
          50           55           60
Leu Val Val Val Ala Glu Ser
          65           70

```

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-2-17

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

CTC ACG GAG CGG CTT TAC TGC GGG GGC CTT ATG TTC AAC AGC AAG GGG      48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1           5           10           15
GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC      96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
          20           25           30
AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA      144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
          35           40           45
AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT      192

```



101

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

TTG GTC GTG GTG GCT GAG AGT 213  
 Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-2-21

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:



CTC ACG GAG CGG CTT TAC TGC GGG GGC CTT ATG TTC AAC AGC AAG GGG 48  
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15  
 GCC CAG TGT GGT TAT CGC CGT TGT CGT GCT AGT GGA GTT CTG CTT ACC 96  
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30  
 AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA 144  
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45  
 AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT 192  
 Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60  
 TTG GTC GTG GTG GCT GAG AGT  
 Leu Val Val Val Ala Glu Ser 213  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15  
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30  
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45  
 Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60  
 Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCG	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CTT TGT GTT CAG GAC GGT AAT	296
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CTT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATG TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CTT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	

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GGA CAC CGA ATG GCT  
Gly His Arg Met Ala  
180

541

## (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 180 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
1 5 10 15  
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
20 25 30  
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
35 40 45  
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
50 55 60  
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
65 70 75 80  
Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
85 90 95  
Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
100 105 110  
Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val Gly  
115 120 125  
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
130 135 140  
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
145 150 155 160  
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
165 170 175  
His Arg Met Ala  
180

## (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 541 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-3-14

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCT CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CCT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACA ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA	526

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Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175

GGA CAC CGA ATG GCT  
 Gly His Arg Met Ala  
 180

541

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15  
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30  
 Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45  
 Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60  
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80  
 Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95  
 Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
 100 105 110  
 Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly  
 115 120 125  
 Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
 130 135 140  
 Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160  
 Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
 165 170 175  
 His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 17 :

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 541 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-21

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CCG AAC ACG TCT GGC CTC TAC GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Glu Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	



GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Phe Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	
GGA CAC CGA ATG GCT	541
Gly His Arg Met Ala	
180	

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	
Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr	
85 90 95	
Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val	
100 105 110	
Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly	
115 120 125	
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala	
130 135 140	
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln	
145 150 155 160	
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly	
165 170 175	
His Arg Met Ala	



180

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR16-9-13

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	45
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	

SUBSTITUTE SHEET (RULE 26)



GGC GCG GCC ACG ATG TGC TCA GCG CTC TAC GTG GGT GAT ATG TGT GGG 430  
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly  
 130 135 140

GCC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT 478  
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His  
 145 150 155

CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 525  
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175

GGA CAT CGA ATG GCT 541  
 Gly His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80

Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val  
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly  
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly



165

170

175

His Arg Met Ala  
180

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-9-20

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	



GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val 115 120 125	382
GGC GCG GCT ACG ATG TGC TCT GCG CTC TAC GTG GGT GAC ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140	430
GCT GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526
GGA CAT CGA ATG GCT Gly His Arg Met Ala 180	541

## (2) INFORMATION FOR SEQ ID NO: 22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80
Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr 85 90 95
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val 100 105 110
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly 115 120 125
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140



Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
165 170 175

His Arg Met Ala  
180

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-1-10

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 2..541

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	45
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	



ACC TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC 334  
 Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr  
 100 105 110  
 GTC GGG GCA ACC ACC GGT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA 382  
 Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
 115 120 125  
 GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG 430  
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly  
 130 135 140  
 GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT 478  
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His  
 145 150 155  
 CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 525  
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175  
 GGA CAT CGC ATG GCT 541  
 Gly His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15  
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30  
 Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45  
 Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60  
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80  
 Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95  
 Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
 100 105 110  
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly



115

120

125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
130 135 140

Val Ph Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
155 170 175

His Arg Met Ala

180

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-19

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

C GTC GGC GGT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCT TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	

SUBSTITUTE SHEET (RULE 26)



GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT 286  
 Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn  
 80 85 90 95

ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC 334  
 Thr Ser Thr Cys Trp Thr Pr Val Thr Pro Thr Val Ala Val Arg Tyr  
 100 105 110

GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA 382  
 Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
 115 120 125

GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG 430  
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly  
 130 135 140

GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT 478  
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His  
 145 150 155

CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 526  
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175

GGA CAT CGA ATG GCT 541  
 Gly His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45

Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80

Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95



Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
 100 105 110  
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly  
 115 120 125  
 Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
 130 135 140  
 Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160  
 Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
 165 170 175  
 His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-1-20

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 2..541

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCT TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	



CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp 65 70 75	238
GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn 80 85 90 95	286
ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr 100 105 110	334
GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val 115 120 125	382
GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140	430
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	479
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526
GGA CAT CGA ATG GCT Gly His Arg Met Ala 180	541

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45
Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

SUBSTITUTE SHEET (RULE 26)



Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly  
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
 165 170 175

His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 287 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HCC1153

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..287

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC	47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala	
1 5 10 15	
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG	95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu	
20 25 30	
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA	143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
35 40 45	
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA	191



Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu  
 50 55 60

CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA 239  
 His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu  
 65 70 75

ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA 297  
 Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser  
 80 85 90 95

## (2) INFORMATION FOR SEQ ID NO: 30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His  
 1 5 10 15

Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr  
 20 25 30

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser  
 35 40 45

Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His  
 50 55 60

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile  
 65 70 75 80

Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser  
 85 90 95

## (2) INFORMATION FOR SEQ ID NO: 31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: HD10-1-25



## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..401

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCC GCA CTC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu	
50 55 60	
GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA	335
Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA	383
Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu	
115 120 125	
ACC TTC TGG CAC AAG CAT	401
Thr Phe Trp His Lys His	
130	

## (2) INFORMATION FOR SEQ ID NO: 32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala
1 5 10 15



Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu  
                   20                                  25                                  30  
 Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys  
                   35                                  40                                  45  
 Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val  
                   50                                  55                                  60  
 Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys  
                   65                                  70                                  75                                  80  
 Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln  
                                   85                                  90                                  95  
 Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln  
                   100                                  105                                  110  
 Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr  
                   115                                  120                                  125  
 Phe Trp His Lys His  
                   130

## (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-1-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	
1                                  5                                  10                                  15	
GCA TGC ATG TCA GGT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20                                  25                                  30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC	143



Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly  
                   35                                  40                                  45  
 TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC 191  
 Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu  
                   50                                  55                                  60  
 GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG 235  
 Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu  
                   65                                  70                                  75  
 TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC 237  
 Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His  
                   80                                  85                                  90                                  95  
 CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA 335  
 Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln  
                                   100                                  105                                  110  
 CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA 353  
 Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu  
                   115                                  120                                  125  
 ACC TTC TGG CAC AAG CAT 401  
 Thr Phe Trp His Lys His  
                   130

## (2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala  
   1                                  5                                  10                                  15  
 Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu  
                   20                                  25                                  30  
 Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys  
                   35                                  40                                  45  
 Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val  
                   50                                  55                                  60  
 Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys  
                   65                                  70                                  75                                  80  
 Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln  
                   85                                  90                                  95  
 Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln



100

105

110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr  
 115 120 125

Phe Trp His Lys His  
 130

## (2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-164

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met 1 5 10 15	47
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu 20 25 30	95
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly 35 40 45	143
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile 50 55 60	191
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu 65 70 75	239
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His 80 85 90 95	287
CAG TTC AAG GGA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA	335

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Gln Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln  
 100 105 110

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG 383  
 Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu  
 115 120 125

GCC TTT TGG CAC AAG CAT 401  
 Ala Phe Trp His Lys His  
 130

## (2) INFORMATION FOR SEQ ID NO: 36:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu  
 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys  
 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val  
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys  
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln  
 85 90 95

Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln  
 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala  
 115 120 125

Phe Trp His Lys His  
 130

## (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-166

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile	
50 55 60	
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTG ATA GCT CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA	315
Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG	383
Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu	
115 120 125	
GCC TTT TGG CAC AAG CAT	401
Ala Phe Trp His Lys His	
130	

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 1             5             10             15
Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
          20             25             30
Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
          35             40             45
Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
          50             55             60
Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
          65             70             75             80
Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
          85             90             95
Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
          100            105            110
Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
          115            120            125
Phe Trp His Lys His
          130

```

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 401 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: BR36-20-165

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:



TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG 47  
Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met  
1 5 10 15

GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG 95  
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu  
20 25 30

CTT GGA GGG GTC CTC GCG GCC CTA GCG GGC TAC TGC TTG TCA GTC GGT 143  
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly  
35 40 45

TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC 191  
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile  
50 55 60

GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG 239  
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu  
65 70 75

TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC 287  
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His  
80 85 90 95

CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA 335  
Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln  
100 105 110

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG 383  
Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu  
115 120 125

GCC TTT TGG CAC AAG CAT 401  
Ala Phe Trp His Lys His  
130

## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu  
20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys  
35 40 45



Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val  
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys  
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln  
 85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln  
 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala  
 115 120 125

Phe Trp His Lys His  
 130

## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-2-1

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..509

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	



50	55	60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC			239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro			
65	70	75	
GGG TAC CTT TGG CCC CTT TAC GCG AAT GAG GGC CTC GGG TGG GCA GGG			287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly			
80	85	90	95
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC			335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp			
100	105	110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG			383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr			
115	120	125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC			431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro			
130	135	140	
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG			479
Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu			
145	150	155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA			509
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu			
160	165		

## (2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp			

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85

90

95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile  
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu  
 165

## (2) INFORMATION FOR SEQ ID NO: 43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-2-6

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..509

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
CGC ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	



CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC 219  
 Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro  
 65 70 75  
 GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG 287  
 Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly  
 80 85 90 95  
 TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC 335  
 Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp  
 100 105 110  
 CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG 383  
 Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr  
 115 120 125  
 TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC 431  
 Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro  
 130 135 140  
 ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG ACG GTC CTT GAG 479  
 Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu  
 145 150 155  
 GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA 509  
 Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu  
 160 165

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95



Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Val Asn Tyr Ala Thr Gly Asn Leu  
 165

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-4-1

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..580

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

A	ACG	TGC	GGA	TTC	GCC	GAT	CTC	ATG	GGG	TAT	ATC	CCG	CTC	GTA	GGC	46
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	
	1				5					10					15	
GGC	CCC	ATT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	GTC	94
Gly	Pro	Ile	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	
				20					25					30		
CTT	GAG	GAC	GGG	GTA	AAC	TAT	GCA	ACA	GGG	AAT	TTA	CCC	GGT	TGC	TCT	142
Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	
			35				40						45			
TTC	TCT	ATC	TTT	ATT	CTT	GCT	CTT	CTC	TGG	TGT	CTG	ACC	GTT	CCG	GCC	190
Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	
			50				55						60			
TCT	GCA	GTT	CCC	TAC	CGA	AAT	GCC	TCT	GGG	ATT	TAT	CAT	GTT	ACC	AAT	238



Ser Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn  
 65 70 75  
 GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA 286  
 Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu  
 80 85 90 95  
 CAC GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA 334  
 His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg  
 100 105 110  
 TGC TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA 382  
 Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala  
 115 120 125  
 GTC ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT 430  
 Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala  
 130 135 140  
 GCC CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC 478  
 Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe  
 145 150 155  
 TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG 526  
 Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val  
 160 165 170 175  
 CAG AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG 574  
 Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg  
 180 185 190  
 ATG GCA 580  
 Met Ala

## (2) INFORMATION FOR SEQ ID NO: 46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly  
 1 5 10 15  
 Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu  
 20 25 30  
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Ile Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60



Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
65 70 75 80

Cys Pr Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His  
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys  
100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val  
115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala  
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met  
180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 580 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: PC-4-6

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC 46  
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly  
 1 5 10 15

GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC 96



Gly Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val	
20 25 30	
CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT	142
Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser	
35 40 45	
TTC TCT ATC TTT ATT CTT GCT CTT CTC TGG TGT CTG ACC GTT CCG GCC	190
Phe Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala	
50 55 60	
TCT GCA GTT CCC TAC CGA AAT GCC TTT GGG ATT TAT CAT GTT ACC AAT	238
Ser Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn	
65 70 75	
GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA	286
Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu	
80 85 90 95	
CAC GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA	334
His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg	
100 105 110	
TGC TGG GTC CAA ATT ACC CCT ACA CTG TCA GCT CCG AGC CTC GGA GCA	382
Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala	
115 120 125	
GTC ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT	430
Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala	
130 135 140	
GCC CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC	478
Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe	
145 150 155	
TTG GTA GGC CAA ATG TTC ACC TAT AGG CTT CGC CAG CAC GCT ACG GTG	526
Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val	
160 165 170 175	
CAG AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG	574
Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg	
180 185 190	
ATG GCA	580
Met Ala	

## (2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear -

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

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Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly  
 1 5 10 15  
 Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu  
 20 25 30  
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His  
 85 90 95  
 Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val  
 115 120 125  
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175  
 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-3-4



## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..959

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr 1 5 10 15	47
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val 20 25 30	95
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg 35 40 45	143
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln 50 55 60	191
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CCG TCC TGG GGT CAA CCC Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro 65 70 75	239
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly 80 85 90 95	287
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp 100 105 110	335
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr 115 120 125	383
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro 130 135 140	431
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu 145 150 155	479
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser 160 165 170 175	527
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala 180 185 190	575
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys 195 200 205	623

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CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC GCA 671  
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala  
210 215 220

CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC TGG 719  
Pro Gly Cys Val Pr Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp  
225 230 235

GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC ACG 767  
Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr  
240 245 250 255

GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC CTC 815  
Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu  
260 265 270

TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG GTA 863  
Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val  
275 280 285

GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG AAC 911  
Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn  
290 295 300

TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG GCA 959  
Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala  
305 310 315

## (2) INFORMATION FOR SEQ ID NO: 50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala  
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly  
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
85 90 95

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Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175  
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val  
 180 185 190  
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro  
 195 200 205  
 Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro  
 210 215 220  
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val  
 225 230 235 240  
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala  
 245 250 255  
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys  
 260 265 270  
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly  
 275 280 285  
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys  
 290 295 300  
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 959 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

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(B) CLONE: PC-1-8

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
CGC ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GSA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	
130 135 140	
GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623

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Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys		
				195				200						205			
CCA	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCA	GAT	AAC	CTG	ATC	CTA	CAC	GCA		671
Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala		
		210					215				220						
CCT	GGT	TGC	GTG	CCT	TGT	GTC	ATG	ACA	GGT	AAT	GTG	AGT	AGA	TGC	TGG		719
Pro	Gly	Cys	Val	Pro	Cys	Val	Met	Thr	Gly	Asn	Val	Ser	Arg	Cys	Trp		
		225				230				235							
GTC	CAA	ATT	ACC	CCT	ACA	CTG	TCA	GCC	CCG	AGC	CTC	GGA	GCA	GTC	ACG		767
Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Leu	Gly	Ala	Val	Thr		
240					245					250					255		
GCT	CCT	CTT	CGG	AGA	GCC	GTT	GAC	TAC	CTA	GCG	GGA	GGG	GCT	GCC	CTC		815
Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	Gly	Gly	Ala	Ala	Leu		
				260				265					270				
TGC	TCC	GCG	TTA	TAC	GTA	GGA	GAC	GCG	TGT	GGG	GCA	CTA	TTC	TTG	GTA		863
Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	Gly	Ala	Leu	Phe	Leu	Val		
		275					280					285					
GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	CGC	CAG	CAC	GCT	ACG	GTG	CAG	AAC		911
Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	Gln	His	Ala	Thr	Val	Gln	Asn		
		290					295				300						
TGC	AAC	TGT	TCC	ATT	TAC	AGT	GGC	CAT	GTT	ACC	GGC	CAC	CGG	ATG	GCA		959
Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	His	Val	Thr	Gly	His	Arg	Met	Ala		
		305				310				315							

## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn		
1				5					10					15			
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly		
		20					25					30					
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Met	Gly	Val	Arg	Ala		
		35				40					45						
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro		
		50				55				60							
Ile	Pro	Lys	Ala	Arg	Gln	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly		
		65			70					75				80			



Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
                             85                            90                            95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
                             100                            105                            110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
                             115                            120                            125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val  
                             130                            135                            140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
                             145                            150                            155                            160  
 Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
                             165                            170                            175  
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val  
                             180                            185                            190  
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro  
                             195                            200                            205  
 Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro  
                             210                            215                            220  
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val  
                             225                            230                            235                            240  
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala  
                             245                            250                            255  
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys  
                             260                            265                            270  
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly  
                             275                            280                            285  
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys  
                             290                            295                            300  
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala  
                             305                            310                            315

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

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(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC C/E:

(ix) FEATURE:

(A) NAME/KEY: JES

(B) LOCATION: 2..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CCATGAGCAC GAATCCTAAA CCTCAAGAA AAACCAAG AAACACCAAC CGTCGCCAC	60
AGGACGTCAA GTTCCCGGGC GGTGGTCAGA TCGTTGGCGG AGTTTACTTG TTGCCGCGCA	120
GGGGCCCTAG GATGGGTGTG CGCSCGACTC GGAAGACTTC GGAACGGTGG CAACCCCGTG	180
GACGGCGTCA GCCTATTCCC AAGGGCGGCT AGCCCGCGG CCGGTCCTGG GGTCAACCTG	240
GGTACCCTTG GCCCCCTTAC GCCAATGAGG GCCTCGGGTG GGCAGGGTGG CTGCTCTCCC	300
CTCGAGGCTC TCGGCCTAAT TGGGGCTCCA ATGACTCCCG GCGAAAATCG CTAATTTGG	360
GTAAGGTCAT CGATACCCTA ACCTGCGGAT TCGCCATCT CATGGGGTAY ATCCCGCTCG	420
TAGGCGGCCC CRTTGGGGGC GTCCCAAGGG CTCTCGCACA CGGTGTGAGG GTCCTTGAGG	480
ACGGGGTAAA CTATSCAACA GGGAAATTAC CCGGTGCTC TTTCTCTATC TTTATTCTTG	540
CTCTTCTCTC GTGTCTGACC GTTCCGGCTT CTGCAGTCC CTACCGAAAT GCCTCTGGGA	600
TTTATCATGT TACCAATGAT TGCCCAACT CTTCATAGT CTATGAGGCA GATAACCTGA	660
TCCTACACGC ACCTGGTTGC GTGCCCTTGT TCATGACAGG TAATGTGAGT AGATGCTGGG	720
TCCAAATTAC CCCTACACTG TCAGCCCCGA GCCTCGGAGC AGTCACGGCT CCTCTTCGGA	780
GAGCCGTGA CTACCTAGCG GGAGGGGCTG CCCTCTGCTC CGCCTTATAC GTAGGAGACG	840
CGTGTGGGGC ACTATTCTTG GTAGGCCAAA TGTTACCTA TAGGCCTCGC CAGCACGCTA	900
CGGTGCAGAA CTGCAACTGT TCCATTTACA GTGGCCATGT TACCGGCCAC CGGATGGCA	959

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1					5				10					15	

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Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175  
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val  
 180 185 190  
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro  
 195 200 205  
 Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro  
 210 215 220  
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val  
 225 230 235 240  
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala  
 245 250 255  
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys  
 260 265 270  
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly  
 275 280 285  
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys  
 290 295 300  
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala  
 305 310 315

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## (2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: PC-1-37

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT      60
TCAGGCGGGC CGCATGACCT GATCATATGC GACGAGTGCC ATTCCAGGA CGCCACCACC      120
ATTCTTGGGA TAGGCACTGT CCTTGACCAG GCAGAGACGG CTGGAGCTAG GTCGTCGTC      180
TTGGCCACGG NCACCCCTCC CGGCACTGTG ACAACGCCCC ACCCCAACAT CGAGGAAGTG      240
GGCCTGCCTC AGGAGGGGGA GGTTCCTTC TACGGCAGAG CCATTCCTCT TGCTTTTATA      300
AAGGGTGGA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA ATTGTGATGA ACTC          354
  
```

## (2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
1           5           10          15
Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val Ile Ile Cys Asp Glu
20          25          30
  
```



Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu  
 35 40 45  
 Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Xaa  
 50 55 60  
 Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val  
 65 70 75 80  
 Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala Ile Pro  
 85 90 95  
 Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys  
 100 105 110  
 Lys Asn Cys Asp Glu Leu  
 115

## (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-48

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT 60  
 TCAGGCGGCG CGTATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCACC 120  
 ATTCTTGGGA TAGGCACTGT CCTTGACCAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC 180  
 TTGGNCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCC ACCCCAACAT CGAGGAAGTG 240  
 GCCCTGCCTC AGGAGGGGGA GGTTCCTTC TACGGNAGAG CCATTCCCCT TGCTTTTATA 300  
 AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAGAAAA AATGTGATGA ACTT 354

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
 1             5             10             15
Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys Asp Glu
      20             25             30
Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
      35             40             45
Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Xaa Thr Xaa
      50             55             60
Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
      65             70             75             80
Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Xaa Arg Ala Ile Pro
      85             90             95
Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
      100             105             110
Lys Lys Cys Asp Glu Leu Arg Gln Ala Thr Asp Gln Pro Gly Arg Glu
      115             120             125
Arg Pro Trp Glu Tyr
      130

```

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 357 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-37

(ix) FEATURE:

(A) NAME/KEY: CDS



(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

ATGGCTTTTCA TGTCTCCGGA CTTGGAGGTC ATTACCANCA CTTGGGTTCT GGTGGGGGGC	60
GTGTGGGGA CCGTTCNCNC CTACTGCTTG ACGGTGGGT CCGTAGCCAT AGTGGGTAGG	120
ATCATCCTCT CTGGGAAACC TGCCATCAAT NCCGATAGGG AGGTATTATA CCAGCAATTT	180
GATGAGATGG AGGAGTGCTC GGCCTCGTTG CCTATATGG ACGAAACACG TNCCTTGCC	240
GGACAATTCA AAGAGAAAGT GCTCGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT	300
CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGATC AGTTCCTGGNC CACATAC	357

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

Met Ala Phe Met Ser Pro Asp Leu Glu Val Ile Thr Xaa Thr Trp Val
1          5          10          15

Leu Val Gly Gly Val Val Ala Thr Leu Xaa Xaa Tyr Cys Leu Thr Val
          20          25          30

Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala
          35          40          45

Ile Ile Xaa Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Gly
          50          55          60

Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Xaa Ile Ala
65          70          75          80

Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln
          85          90          95

Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala
          100          105          110

Asp Gln Phe Trp Xaa Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-48

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

ATGGCTTGCA TGTCTGCCGA CTTGGAGGTC ATTACCANCA CTTGGGTTCT GGTGGGGGGC	60
GTGTGTGGCGN CCCTGGCGGC CTAATGCTTG ACGGTGGGTT CGGTAGCCAT AGTCGGTAGG	120
ATCATCTTCT CTGGGAACCC TGCCATCAT CCCGATAGGG AGGCATTATA CCANCAATTT	180
GATGAGATGG AGGAGTGCTC GGCTTCGTTG CCTATATGG ACGAGACAG TGCCATTGCC	240
GGACAATTCA AAGAGAAAGT GGTGGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT	300
CTGAAGCCCG CAGCCACGTC TGTGTGGAAC AAGGCTGANC AGTTCTGGGC CACATAC	357

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Met	Ala	Cys	Met	Ser	Ala	Asp	Leu	Glu	Val	Ile	Thr	Xaa	Thr	Trp	Val
1			5						10					15	
Leu	Val	Gly	Gly	Val	Val	Ala	Xaa	Leu	Ala	Ala	Tyr	Cys	Leu	Thr	Val
		20						25					30		
Gly	Ser	Val	Ala	Ile	Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Lys	Pro	Ala
		35				40					45				
Ile	Ile	Pro	Asp	Arg	Glu	Ala	Leu	Tyr	Xaa	Gln	Phe	Asp	Glu	Met	Glu
	50					55					60				

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Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala  
 65 70 75 80  
 Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln  
 85 90 95  
 Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala  
 100 105 110  
 Xaa Gln Phe Trp Ala Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO: 63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP:161"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGGAGGCC AGGAGAGTGA TCTCCTCC

28

## (2) INFORMATION FOR SEQ ID NO: 64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP:162"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGGCTGCTCT ATCCTCATCG ACGCCATC

28

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP153"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GCCAGAGGCT CGGAAGGCCA TCAGCGCT

28

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP164"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGCTGCTCT GTCCTCCTCG ACGCCGCA

28

(2) INFORMATION FOR SEQ ID NO: 67:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP=23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTCATGGGGT ACATTCCGCT

20

## (2) INFORMATION FOR SEQ ID NO: 68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP=54"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTATTACCAG TTCATCATCA TATCCCA

27

## (2) INFORMATION FOR SEQ ID NO: 69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl16"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TTTTAAATAC ATCATGCTG YATG

24

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl66"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CTATTATTGT ATCCCRCTGA TGAARTCCA CAT

33

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc\_feature



(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl18:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ACTAGTCGAC TAYTGATCCR CTATRWARTT CCACAT

36

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl17:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TTTTAAATAC ATCGCRCTGC ATGCA

25

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl19:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ACTAGTCGAC TARTTGCATA GCCKRTTCAT CCAYTG

36



## (2) INFORMATION FOR SEQ ID NO: 74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl31:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GGAATTCTAG ACCTCTGGGA YGARAYTGGA ARTG

34

## (2) INFORMATION FOR SEQ ID NO: 75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl30:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GGAATTCTAG ACGCTAYCAR GCACGTTGYG C

31

## (2) INFORMATION FOR SEQ ID NO: 76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (gen mic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURES:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP:134:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CATATAGATG CCCACTTCCT ATC

23

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP:3:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTGTGCCAGG ACCATC

16

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPr4:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GACATGCATG TCATGATGTA

20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP=152:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TACGCCTCTT CTATATCGGT TGGGGCCTG

29

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO



## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPPr52:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ATGTTGGGTA AGGTCATCGA TACCCT

26

## (2) INFORMATION FOR SEQ ID NO: 81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPPr41:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCCGGGAGGT CTCGTAGACC GTGCA

25

## (2) INFORMATION FOR SEQ ID NO: 82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iii) ANTI-SENSE: YES

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPPr40:



(xi) SEQUENCE DESCRIPTION; SEQ ID NO: 82:

CTATTAAAGA TAGAGAAAGA GCAACCGGG

29

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 223 of the V2 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	His	Thr
1				5				10		

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 233 of the V2 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala
1				5				10		

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV  
type 3



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Val Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Val Met. Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Val Arg Tyr Val Gly Ala Thr Thr Ala Ser  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 : 257 of the V4 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ala	Pro	Ser	Leu	Gly	Ala	Val	Thr	Ala	Pro
1				5					10

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Arg	Pro	Arg	Arg	His	Gln	Thr	Val	Gln	Thr
1				5					10

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:



Arg Pro Arg Gln His Ala Thr Val Gln Asn  
1                   5                   10

1

5

10

(2) INFORMATION FOR SEQ ID NO: 93:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 70 to 78 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Pro Thr Gly Arg Ser Thr Gly Gln  
1 5

1

**5**

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR33 and BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Val Gln Asp Gly Asn Thr Ser Thr  
1 5

1

5

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Val Gln Asp Gly Asn Thr Ser Ala  
1 5

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36







Ser Gln Ala Ala Pro Tyr Il Glu Gln Ala Gln Val Ile Ala His Gln  
1 5 10 15  
Phe Lys Glu Lys  
20

## (2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL ISOLATE: BR36
- (viii) POSITION IN GENOME:
  - (B) MAP POSITION: positions 1724 to 1743 of HCV type 3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ile Ala His Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala  
1 5 10 15  
Thr Gln Gln Gln  
20

## (2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL ISOLATE: HD10
- (viii) POSITION IN GENOME:
  - (B) MAP POSITION: positions 1724 to 1743 of HCV type 3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Ile Ala His Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala  
1 5 10 15



Thr Gln Gln Gln  
20

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Leu	Ser	Gly	Lys	Pro	Ala	Ile	Ile	Pro	Asp	Arg	Glu	Ala	Leu	Tyr	Gln
1				5				10						15	
Gln Phe Asp Glu															
20															

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

Leu	Ser	Gly	Lys	Pro	Ala	Ile	Ile	Pro	Asp	Arg	Glu	Val	Leu	Tyr	Gln
1				5				10						15	
Gln Phe Asp Glu															
20															

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: position 1712 to 1731 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Ser	Ala	Ser	Leu	Pro	Tyr	Met	Asp	Glu	Thr	Arg	Ala	Ile	Ala	Gly	Gln
1			5					10						15	

Phe	Lys	Glu	Lys
			20

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

Ile	Ala	Gly	Gln	Phe	Lys	Glu	Lys	Val	Leu	Gly	Phe	Ile	Ser	Thr	Thr
1				5				10						15	

Gly	Gln	Lys	Ala
			20

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB48-3-10

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTC TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GCA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC ACC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGT CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AAA	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys	
65 70 75	
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG	286
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC GCT GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA CCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu	
100 105 110	
GGA GCC	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15

SUBSTITUTE SHEET (RULE 26)



Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala L u Thr  
                   20                                  25                                  30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu  
                   35                                  40                                  45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
                   50                                  55                                  60  
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys Ala  
                   65                                  70                                  75                                  80  
 Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                   85                                  90                                  95  
 Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu Gly  
                   100                                  105                                  110

Ala

## (2) INFORMATION FOR SEQ ID NO: 108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: G3116-3-5

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTA TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1                                  5                                  10                                  15	
CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AGA GCA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu	
20                                  25                                  30	
ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AGG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp	
35                                  40                                  45	



CTG TGC GGG TAT CGC AGA TGC CGT GCG AGC GGC GTC TAC ACC ACC AGC 190  
 Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser  
           50                          55                          60

TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCT ATC AGA 238  
 Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg  
           65                          70                          75

GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG 286  
 Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu  
           80                          85                          90                          95

GTC GTC ATT GCT GAA AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC 334  
 Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu  
                           100                          105                          110

GGA GCC 340  
 Gly Ala

## (2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln  
   1                          5                          10                          15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu Thr  
           20                          25                          30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu  
           35                          40                          45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
           50                          55                          60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala  
           65                          70                          75                          80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                           85                          90                          95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly  
           100                          105                          110

Ala

## (2) INFORMATION FOR SEQ ID NO: 110:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: GB215-3-8

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

C TCC ACT GTA ACC GAA AAA GAC ATC AGG GTC GAG GAG GAG GTA TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GTA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAT AGC AAA GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCC ATC AGG	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCG TCA GGG CTG AGA GAC TGC ACT ATG CTG GTC TAT GGT GAC GAC CTG	286
Ala Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATT GCC GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GTC	340
Gly Val	

(2) INFORMATION FOR SEQ ID NO: 111:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
 1             5             10             15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
      20             25             30
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
      35             40             45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
      50             55             60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
      65             70             75             80
Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu Val
      85             90             95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
      100             105             110
Val

```

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: GB358-3-3

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTG TAT

46

SUBSTITUTE SHEET (RULE 26)



Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr  
 1 5 10 15

CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AAG GCA ATT ACT GCC CTA 94  
 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu  
 20 25 30

ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC 142  
 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp  
 35 40 45

CTG TGT GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC 190  
 Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser  
 50 55 60

TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AGA 238  
 Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg  
 65 70 75

CGC GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG 286  
 Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu  
 80 85 90 95

GTC GTC ATC GCT GAG AGC GAT GGC GTT GAG GAG GAC AAA CGA GCC CTC 334  
 Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu  
 100 105 110

GGA GCC 340  
 Gly Ala

## (2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln  
 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu Thr  
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu  
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala  
 65 70 75 80

SUBSTITUTE SHEET (RULE 26)



Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95  
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly  
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GB549-3-6

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

C TCC ACG GTG ACC GAA AGG GAT ATC AGG ACC GAG GAA GAG ATC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr	
1 5 10 15	
CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	
CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC	190
Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG	238
Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg	
65 70 75	
GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA	286
Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	



GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC 334  
 Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu  
                   100                  105                  110

CGA GCC 340  
 Arg Ala

## (2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln  
   1                  5                  10                  15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr  
           20                  25                  30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu  
           35                  40                  45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
           50                  55                  60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala  
           65                  70                  75                  80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val  
                   85                  90                  95

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg  
           100                  105                  110

Ala

## (2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO



(vii) IMMEDIATE SOURCE:

(B) CLONE: G3809-3-1

(ix) **FEATURES:**

(A) NAME/KEY: CDS

(B) LOCATION: 2...340

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

C TCC ACT GTG ACT GAG AGA GAC ATC AAG GTC GAA GAA GAA GTC TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA GCC GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu	
20 25 30	
ACG GAG AGA CTC TAC GTG GGC GGC CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTT TGC GGG TAT CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA ATG ACG TGC TAC CTT AAG GCC TCA GCA GCC ATC AGG	238
Phe Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCT GCG GGG CTA AAG GAT TGC ACC ATG CTG GTT TGC GGT GAC GAC CTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTG ATC GCC GAG AGC GGT GGC GTT GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GCT	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr Gln  
1 5 10 15



Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu Thr  
           20                                  25                                  30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu  
           35                                  40                                  45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
           50                                  55                                  60  
 Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala  
           65                                  70                                  75                                  80  
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                                   85                                  90                                  95  
 Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly  
                                   100                                  105                                  110  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB358-4-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1                                  5                                  10                                  15	
CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20                                  25                                  30	
GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35                                  40                                  45	



TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC	240
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His	
85 90 95	
CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro	
115 120 125	
CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT	432
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTC TTG	480
Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	
145 150 155 160	
GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG	528
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG A	574
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg	
180 185 190	

## (2) INFORMATION FOR SEQ ID NO: 119:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	

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50

55

60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His Hi Ile Leu His  
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr  
130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg  
180 185 190

## (2) INFORMATION FOR SEQ ID NO: 120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: GB549-4-3

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACG	TGC	GGC	TTT	GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	CTC	GTG	GGC	GCC	48
Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	
1				5				10					15			
CCT	GTG	GGT	GGC	GTC	GCC	AGG	GCC	TTG	GCA	CAT	GGT	GTC	AGG	GCC	GTG	96
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val	
			20				25					30				

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GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC	240
Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His	
85 90 95	
CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys	
100 105 110	
TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG	384
Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro	
115 120 125	
CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC	432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG	480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	
145 150 155 160	
GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CGC CAT TGG ACT ACC CAG	528
Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA A	574
Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg	
180 185 190	

## (2) INFORMATION FOR SEQ ID NO: 121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30



Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys  
 100 105 110  
 Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro  
 115 120 125  
 Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg  
 180 185 190

## (2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 574 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB809-4-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC

49



Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 CCC GTT GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG 96  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 GAG GAC GGG ATT AAC TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC 144  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 TCT ATC TTC CTC CTG GCA CTT CTT TCG TGC CTC ACT GTC CCA GCG TCA 192  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 GCT GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC AAT GAC 240  
 Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80  
 TGT CCG AAT TCC AGC GTA GTC TAT GAA ACT GAC CAC CAT ATA TTG CAC 288  
 Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His  
 85 90 95  
 TTG CCG GGG TGC GTA CCC TGC GTG AGG GCC GGG AAC GTG TCT CGT TGC 336  
 Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys  
 100 105 110  
 TGG ACG CCG GTA ACA CCT ACG GTG GCT GCC GTA TCC ATG GAC GCT CCG 384  
 Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro  
 115 120 125  
 CTC GAG TCC TTC CCG CCG CAT GTG GAC CTA ATG GTA GGT GCG GCC ACC 432  
 Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 GTG TGT TCT GTC CTC TAT GTT GGA GAC CTC TGT GGA GGT GCT TTC CTA 480  
 Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu  
 145 150 155 160  
 GTG GGG CAG ATG TTC ACC TTC CAG CCG CGT CGC CAC TGG ACC ACG CAG 528  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 GAT TGT AAT TGC TCC ATC TAT ACT GGC CAT ATC ACC GGC CAC AGG A 574  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg  
 180 185 190

## (2) INFORMATION FOR SEQ ID NO: 123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:



Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pr Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Ph  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro  
 115 120 125  
 Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg  
 180 185 190

## (2) INFORMATION FOR SEQ ID NO: 124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer HCP:206"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:



TGGGGATCCC GTATGATACC CGCTGCTTTG A

31

## (2) INFORMATION FOR SEQ ID NO: 125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer HcPr207"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GGCGGAATTC CTGGTCATAG CCTCCGTGAA

30

## (2) INFORMATION FOR SEQ ID NO: 126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid  
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid  
(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Tyr Glu Thr Glu His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: amino acid
  - (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Val	Tyr	Glu	Ala	Asp	His	His	Ile	Met	His	Leu
1					5					10

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: amino acid
  - (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Val	Tyr	Glu	Thr	Asp	His	His	Ile	Leu	His	Leu
1					5					10

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: amino acid
  - (C) INDIVIDUAL ISOLATE: GB358



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Val Arg Thr Gly Asn Thr Ser Arg Cys Trp Val Pro Leu  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Val Arg Ala Gly Asn Val Ser Arg Cys Trp Thr Pro Val  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Ala Val Ser Met Asp Ala Pro Leu Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 138:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: GB358 and GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:

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- (A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: G8549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CCAGGTACAA CCGAACCAAT TGCC

24

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 957 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..957

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACT AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTA TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACG AGG AAA ACT TCC GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAA GAT CGG CGC CCC ACT GGC AAG TCC TGG GGA AAA CCA GGA	240
Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTG TAC GGG AAT GAG GGC CTC GGC TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCC CCC CGA GGG TCT CGC CCG TCA TGG GGC CCA ACT GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CAC AGG TCA CGC AAC TTG GGT AAG GTC ATC GAT ACC CTT ACG TGT	384
Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTT GCC GAC CTC ATG GGG TAC ATC CCT GTC GTC GGC GCC CCA GTT	432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val	
130 135 140	
GGT GGT GTC GCC AGA GCT CTC GCG CAT GGC GTG AGA GTT CTG GAA GAC	480
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	
145 150 155 160	

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GGG ATA AAC TAT GCA ACA GGG AAC TTG CCC GGT TGC TCC TTT TCT ATC Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175	528
TTC TTA TTG GCC CTG CTA TCT TGT ATC ACT GTG CCG GTC TCC GGC TTG Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu 180 185 190	576
CAG GTC AAG AAC ACC AGC AGC TCT TAC ATG GTA ACC AAT GAC TGC CAG Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val Thr Asn Asp Cys Gln 195 200 205	624
AAC AGT AGC ATC GTC TGG CAG CTC AGG GAT GCT GTT CTT CAC GTC CCC Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro 210 215 220	672
GGG TGT GTC CCT TGT GAG GAG AAG GGC AAC ATA TCC CGC TGT TGG ATA Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile 225 230 235 240	720
CCG GTT TCG CCC AAT ATA GCT GTG AGC CAA CCT GGT GCG CTT ACC AAG Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys 245 250 255	768
GGC CTG CGG ACG CAT ATT GAT ACC ATC ATT GCA TCC GCT ACG TTT TGC Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys 260 265 270	816
TCT GCC CTG TAC ATA GGA GAC CTG TGT GGC GCG GTG ATG TTG GCT TCT Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser 275 280 285	864
CAA GTC TTC ATC ATC TCG CCC CAG CAT CAT AAG TTT GTC CAG GAC TGC Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys 290 295 300	912
AAC TGT TCC ATA TAC CCA GGC CAC ATC ACT GGA CAT CGG ATG GCG Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala 305 310 315	957

## (2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30



Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
 100 105 110  
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175  
 Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu  
 180 185 190  
 Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val Thr Asn Asp Cys Gln  
 195 200 205  
 Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro  
 210 215 220  
 Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile  
 225 230 235 240  
 Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys  
 245 250 255  
 Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys  
 260 265 270  
 Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser  
 275 280 285  
 Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys  
 290 295 300  
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala  
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 1-5:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 2..337

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

C TCA ACG GTC ACG GAG AGG GAC ATC AGA ACT GAG GAG TCC ATA TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CTT GCT TGC TCT TTA CCC GAG CAG GCA CGG ACT GCC ATA CAC TCA CTG	94
Leu Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu	
20 25 30	
ACT GAG AGG CTT TAC GTG GGA GGG CCC ATG CTA AAC AGC AAA GGG CAA	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln	
35 40 45	
ACC TGC GGA TAC AGA CGC TGC CGC GCC AGC GGA GTG TTC ACC ACT AGC	190
Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGA AAT ACC ATC ACG TGC TAC GTG AAG GCA CAA GCA GCC TGT AAG	238
Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys	
65 70 75	
GCT GCG GGC ATA ATT GCC CCC ACG ATG CTG GTG TGC GGC GAC GAT CTA	286
Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC TCA GAG AGT CAG GGG ACC GAG GAG GAC GAG CGG AAC CTA	334
Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
 1             5             10             15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
      20             25             30
Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln Thr
      35             40             45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
      50             55             60
Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys Ala
      65             70             75             80
Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
      85             90             95
Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
      100            105            110
Ala

```

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..345

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ATG AGC ACA CTT CCT AAA CCA CAA AGA AAA ACC AAA AGA AAC ACC AAC

48



Met Ser Thr Leu Pro Lys Pr Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 CCC GGC CAC AGG ACG TTA AGT TCC CAG GCG GCG GTC AGA TCG TTG GTG 96  
 Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val  
 20 25 30  
 GAG TTT ACG TGC TAC CAC GCA GGG GCC CCC AGT TGG GTG TGC GTG CAG 144  
 Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln  
 35 40 45  
 TGC GCA AGA CTT CCG AGC GGT CGC AAC CTC GCA GTA GGC GCC AAC CCA 192  
 Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro  
 50 55 60  
 TCC CCA GGG CGC GCC GAA CCG AGG GCA GGT CCT GGG CTC AGC CCG GGT 240  
 Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly  
 65 70 75 80  
 ACC CTT GGC CCC TAT ATG GGA ATG AGG GCT GCG GGT GGG CAG GGT GGC 288  
 Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly  
 85 90 95  
 TCC TGT CCC CGC GCG GCT CTC GCC CGT CGT GGG GCC CAA ATG ACC CCC 336  
 Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Gln Met Thr Pro  
 100 105 110  
 GGC GCA GGA 345  
 Gly Ala Gly  
 115

## (2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val  
 20 25 30  
 Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln  
 35 40 45  
 Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro  
 50 55 60  
 Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly  
 65 70 75 80  
 Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly

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85

90

95

Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Gln Met Thr Pro  
100 105 110

Gly Ala Gly  
115

## (2) INFORMATION FOR SEQ ID NO: 149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..280

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..277

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

G GCC TGT GAC CTC AAG GAC GAG GCT AGG AGG GTG ATA ACT TCA CTC	46
Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu	
1 5 10 15	
ACG GAG CGG CTT TAC TGT GGT GGT CCT ATG TTC AAC AGC AAG GGA CAA	94
Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln	
20 25 30	
CAC TGC GGT TAC CGC CGC TGC CGT GCT AGT GGG GTG CTA CCC ACC AGC	142
His Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser	
35 40 45	
TTC GGG AAC ACA ATC ACC TGT TAC ATC AAA GCA AAG GCA GCT ACC AAA	190
Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys	
50 55 60	
GCT GCC GGA ATT AAA AAT CCA TCA TTC CTT GTC TGC GGA GAT GAC TTG	238
Ala Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu	
65 70 75	
GTC GTG ATT GCT GAG AGT GCA GGG ATC GAT GAG GAC AGA GCG	280
Val Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala	
80 85 90	

## (2) INFORMATION FOR SEQ ID NO: 150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
 1             5             10             15
Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
          20             25             30
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
          35             40             45
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
          50             55             60
Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
          65             70             75             80
Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala
          85             90

```

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 499 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..499

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC      48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1             5             10             15
CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGC      96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
          20             25             30

```



GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala	
35 40 45	
ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pr Arg Gly Arg Arg Gln Pr	
50 55 60	
ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC GGG	240
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp	
85 90 95	
CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro	
100 105 110	
CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC	384
Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT	432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile	
130 135 140	
GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC	480
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	
145 150 155 160	
GGG GTA AAC TAT GCA ACA G	499
Gly Val Asn Tyr Ala Thr	
165	

## (2) INFORMATION FOR SEQ ID NO: 152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala	
35 40 45	



Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Gln Pr Thr Gly Arg Ser Trp Gly Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Val Asn Tyr Ala Thr  
 165

## (2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ACG TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC	144



Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCG TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT	240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC	298
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His	
85 90 95	
GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC	336
Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys	
100 105 110	
TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC	384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val	
115 120 125	
ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC	432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala	
130 135 140	
CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG	528
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln	
165 170 175	
AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG	576
Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met	
180 185 190	
GCG	579
Ala	

## (2) INFORMATION FOR SEQ ID NO: 154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15



Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu  
                   20                                  25                                  30  
 Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe  
                   35                                  40                                  45  
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
                   50                                  55                                  60  
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
                   65                                  70                                  75                                  80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His  
                                   85                                  90                                  95  
 Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys  
                                   100                                  105                                  110  
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val  
                   115                                  120                                  125  
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala  
                   130                                  135                                  140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
                   145                                  150                                  155                                  160  
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
                                   165                                  170                                  175  
 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met  
                                   180                                  185                                  190

Ala

## (2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC	144
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT	240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	
85 90 95	
GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC	336
Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys	
100 105 110	
TGG GTC CAA ATT ACC CCC ACG CTG TCA GCC CCG AGC TTC GGA GCA GTC	384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val	
115 120 125	
ACG GCT CCC CTT CGG AGA GCC GTT GAT TAC TTG GTG GGA GGG GCT GCC	432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala	
130 135 140	
CTC TGC TCC GCG TTA TAC GTT GGA GAC GCG TGT GGG GCA CTA TTT TTG	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAT GCT ACG GTG CAG	528
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln	
165 170 175	
GAC TGC AAC TGT TCC ATC TAC AGT GGC CAC GTC ACC GGC CAT CAG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met	
180 185 190	
GCA	579
Ala	

## (2) INFORMATION FOR SEQ ID NO: 156:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu  
 20 25 30  
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His  
 85 90 95  
 Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys  
 100 105 110  
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val  
 115 120 125  
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met  
 180 185 190  
 Ala

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 530 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..530

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 3..527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CA CCT ACG ACA GCT CTG CTG GTG GCC CAG TTA CTG CGG ATT CCC CAA	47
Pro Thr Thr Ala Leu Val Ala Gln Leu Arg Ile Pro Gln	
1 5 10 15	
GTG GTC ATT GAC ATC ATC GCA GGG AGC CAC TGG GGG GTC TTG TTT GCC	95
Val Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala	
20 25 30	
GCC GCA TAC TAT GCA TCG GTG GCT AAC TGG ACC AAG GTC GTG CTG GTC	143
Ala Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val	
35 40 45	
TTG TTT CTG TTT GCA GGG GTT GAT GCT ACT ACC CAG ATT TCG GGC GGC	191
Leu Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly	
50 55 60	
TCC AGC GCC CAA ACG ACG TAT GGC ATC GCC TCA TTT ATC ACC CGC GGC	239
Ser Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly	
65 70 75	
GCG CAG CAG AAA CTG CAG CTC ATA AAT ACC AAC GGA AGC TGG CAC ATC	287
Ala Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile	
80 85 90 95	
AAC AGG ACC GCC CTT AAT TGT AAT GAC AGC CTC CAG ACT GGG TTC ATA	335
Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile	
100 105 110	
GCC GGC CTC TTC TAC TAC CAT AAG TTC AAC TCT TCT GGA TGC CCG GAT	383
Ala Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp	
115 120 125	
CGG ATG GCT AGC TGT AGG GCC CTT GCC ACT TTT GAC CAG GGC TGG GGA	431
Arg Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly	
130 135 140	
ACT ATC AGC TAT GCC AAC ATA TCG GGT CCC AGT GAT GAC AAA CCA TAT	479
Thr Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr	
145 150 155	
TGC TGG CAC TAT CCC CCA CGG CCG TGC GGA GTG GTG CCA GCC CAA GAG	527



Cys Trp His Tyr Pro Pro Arg Pr Cys Gly Val Val Pro Ala Gln Glu  
160 165 170 175

GTC  
Val

530

## (2) INFORMATION FOR SEQ ID NO: 158:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln Val  
1 5 10 15  
Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala Ala  
20 25 30  
Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val Leu  
35 40 45  
Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly Ser  
50 55 60  
Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly Ala  
65 70 75 80  
Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn  
85 90 95  
Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile Ala  
100 105 110  
Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp Arg  
115 120 125  
Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly Thr  
130 135 140  
Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr Cys  
145 150 155 160  
Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu Val  
165 170 175

## (2) INFORMATION FOR SEQ ID NO: 159:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

C TCG ACC GTT ACC GAA CAT GAC ATA ATG ACC GAA GAG TCC ATT TAC	46
Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CAA TCA TGT GAC TTG CAG CCC GAG GCA CGC GCA GCA ATA CGG TCA CTC	94
Gln Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu	
20 25 30	
ACC CAA CGC CTC TAC TGT GGA GGC CCC ATG TAC AAC AGC AAG GGG CAA	142
Thr Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln	
35 40 45	
CAG TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTT TTC ACC ACC AGT	190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGC AAC ACC ATG ACG TGC TAC ATC AAG GCT TTA GCC TCC TGT AGA	238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg	
65 70 75	
GCC GCA AGG CTC CGG GAC TGC ACG CTC CTG GTG TGT GGT GAC GAT CTT	286
Ala Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTG GCC ATC TGC GAG AGC CAG GGS ACA CAC GAG GAT GAA GCA AGC CTG	334
Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu	
100 105 110	
AGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 160:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr Gln  
 1 5 10 15  
 Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu Thr  
 20 25 30  
 Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met  
 50 55 60  
 Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg Ala  
 65 70 75 80  
 Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu Arg  
 100 105 110  
 Ala

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

C TCA ACC GCC ACC GAA CAT GAC ATA TTG ACT GAA GAG TCC ATA TAC  
 Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr

46



1	5	10	15	
CAA TCA TGT GAC TCG CAG CCC GAC GCA CGC GCA GCA ATA CGG TCA CTC				94
Gln Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu				
20	25	30		
ACC CAA CGC TTG TTC TGT GGA GGC CCC ATG TAT AAC AGC AAG GGG CAA				142
Thr Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln				
35	40	45		
CAA TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTC TTC ACC ACC AGT				190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser				
50	55	60		
ATG GGC AAC ACC ATG ACG TGC TAC ATT AAG GCT TTA GCC TCC TGT AGA				238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg				
65	70	75		
ACC GCT GGG CTC CGG GAC TAC ACG CTC CTG GTG TGT GGT GAC GAT CAT				286
Thr Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His				
80	85	90	95	
GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCG AAC CTG				334
Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu				
100	105	110		
AGA GCC				340
Arg Ala				

## (2) INFORMATION FOR SEQ ID NO: 162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr Gln			
1	5	10	15
Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu Thr			
20	25	30	
Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln			
35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met			
50	55	60	
Gly Asn Thr Met Thr Cys Tyr Ile-Lys Ala Leu Ala Ser Cys Arg Thr			
65	70	75	80
Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His Val			
85	90	95	



Ala Il Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu Arg  
100 105 110

Ala

## (2) INFORMATION FOR SEQ ID NO: 153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..499

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..496

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ATG AGC ACG AAT CCT AAA CTT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGT GGT GGC CAG ATC GTT GGC	96
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGG CGC CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCG CGC CGA TCC GAG GGC AGA TCC TGG GCG CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	
65 70 75 80	
TAT CCT TGG CCC CTT TAC GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG	298
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCC CCT CGC GGG TCT CGG CCG TCT TGG GGC CCT AAT GAT CCC	336



Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pr Asn Asp Pro  
 100 105 110  
 CGG CGG AGG TCC CGC AAC CTG GGT AAG GTC ATC GAT ACC CTA ACA TGC 384  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC CCC GTC 432  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val  
 130 135 140  
 GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG GAA GAC 480  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
 145 150 155 160  
 GGG ATC AAC TAC GCA ACA G 499  
 Gly Ile Asn Tyr Ala Thr  
 165

## (2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val  
 130 135 140

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Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
 145 150 155 160

Gly Ile Asn Tyr Ala Thr  
 165

## (2) INFORMATION FOR SEQ ID NO: 155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACSTA ACACCAACCG CCGCCCTATG	60
GACGTTAAGT TCCCAGGCGG TGGTCAGATC GTTGGCGGAG TTTACTTGTT GCCCGGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTGCGA ACCTCGTGGG	180
AGGCGCCAAC CTATCCCCAA GCGCGCGCGA ACCGAGGGCA GATCCTGGGC GCAGCCCCGG	240
TATCCTTGGC CCCTTTACGG CAATGAGGGC TGTGGGTGGG CAGGGTGGCT CCTGTCCCCC	300
CGCGGNTCTC GGNCGTCTTG GGGCCCCAAT GATCCCCGGN GGAGATCCCG CAACTTGGGT	360
AAGGTCATCG ATACCCTAAC ATGCGGCTTC GCCGACCTCA TGGGATACAT CCGGCTTGTA	420
GGCGCCCCCG TGGGTGGCGT CGCCAGGGCC CTGGCACATG GTGTTAGGGC TGTGGAAGAC	480
GGGATCAATT ATGCAACAG	499

## (2) INFORMATION FOR SEQ ID NO: 166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn



215

1	5	10	15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Glu Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	
Leu Leu Ser Pro Arg Xaa Ser Arg Xaa Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu			
115	120	125	

## (2) INFORMATION FOR SEQ ID NO: 167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGG GCC-CTG GCA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATC AAT TAT GCA ACA GGG AAC CTT CCC GGT TGC TCC TTT	144



Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GCG CTC CTC TCG TGC CTG ACT GTT CCC ACA TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC GTT AAC TAT CGC AAT GCT TCG GGC ATT TAT CAC ATC ACC AAT GAC	240
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT GCA AGC ATA GTG TAC GAG ACC GAA AAT CAC ATC TTA CAC	288
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His	
85 90 95	
CTC CCA GGG TGC GTA CCC TGT GTG AGG ACT GGG AAC CAG TCG CGG TGT	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACA GTA GCG TCG CCA TAC GCC GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro	
115 120 125	
CTT GAG CCC TTG CGG CGT CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC	432
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
ATG TGT TCC GCC CTC TAC ATC GGC GAC TTG TGC GGT GGC TTA TTC TTG	480
Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu	
145 150 155 160	
GTG GGC CAA ATG TTC ACC TTC CAA CCG CGA CGT CAC TGG ACC ACT CAG	528
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGC AAT TGT TCC ATC TAC ACG GGC CAC ATT ACG GGT CAT CGG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met	
180 185 190	
GCA	579
Ala	

## (2) INFORMATION FOR SEQ ID NO: 158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15



Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
                   20                                  25                                  30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys S r Phe  
                   35                                  40                                  45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
                   50                                  55                                  60  
 Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
                   65                                  70                                  75                                  80  
 Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His  
                                   85                                  90                                  95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys  
                                   100                                  105                                  110  
 Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro  
                   115                                  120                                  125  
 Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
                   130                                  135                                  140  
 Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu  
                   145                                  150                                  155                                  160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
                                   165                                  170                                  175  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
                   180                                  185                                  190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATC AAC TAC GCA ACA GGG AAT CTC CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GCA CTT CTC TCG TGC CTC ACT GTT CCC GCG TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GGC GTT AAC TAT CGC AAT GCT TCG GGC GTT TAT CAC ATC ACC AAC GAC	240
Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT GCG AGC ATA GTG TAC GAG ACC GAC AAT CAC ATC TTA CAC	288
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His	
85 90 95	
CTC CCA GGG TGC GTA CCC TGT GTG AAG ACC GGG AAC CAG TCG CGG TGT	336
Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACA GTG GCG TCG CCT TAC GTC GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro	
115 120 125	
CTC GAG CCC TTG CCG CGC CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC	432
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
GTG TGC TCC GCC CTC TAC GTC GGC GAC CTG TGC GGT GGC TTA TTC TTG	480
Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TTC CAA CCG CGA CGC CAC TGG ACG ACC CAG	528
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGT AAT TGT TCC ATC TAC GCA GGG CAT ATT ACG GGC CAT CGG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met	
180 185 190	
GCT	579
Ala	

## (2) INFORMATION FOR SEQ ID NO: 170:

SUBSTITUTE SHEET (RULE 26)



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1             5             10             15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
      20             25             30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
      35             40             45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
      50             55             60

Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp
      65             70             75             80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His
      85             90             95

Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys
      100            105            110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro
      115            120            125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
      130            135            140

Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu
      145            150            155            160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
      165            170            175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met
      180            185            190

Ala

```

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 579 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..579

## (ix) FEATURE:

(A) NAME/KEY: mac\_peptide

(B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTT GGT GGC GTC GCC AGA GCC CTT GCG CAC GGC GTC AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATT AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAC CAC CTC ACC AAT GAC	240
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp	
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GTC CAT CAC ATC TTG CAC	288
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His	
85 90 95	
CTT CCA GGA TGC GTC CCT TGT GTA AGA ACT GGG AAC CAG TCT CGG TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTA GCC TTG ACC CCC ACG CTG GCC GCG CCA TAC CTT GGC GCT CCA	384
Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro	
115 120 125	
CTC GAG TCC ATG CGG CGT CAC GTG GAT TTG ATG GTG GGC ACT GCT ACA	432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr	
130 135 140	
TTG TGC TCA GCA CTC TAC GTT GGG GAC CTG TGC GGG GGC ATA TTC CTA	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu	
145 150 155 160	
GCG GGC CAG ATG TTC ACC TTC CGG CCC CGC CTC CAT TGG ACC ACC CAG	528
Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln	
165 170 175	

SUBSTITUTE SHEET (RULE 26)



GAG TGC AAT TGT TCC ACC TAT CCG GGC CAC ATC ACG GGT CAT AGA ATG 576  
 Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met  
                   180                  185                  190

GCG 579  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
   1                  5                  10                  15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
                   20                  25                  30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
                   35                  40                  45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
   50                  55                  60

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp  
   65                  70                  75                  80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His  
                   85                  90                  95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys  
                   100                  105                  110

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro  
                   115                  120                  125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr  
                   130                  135                  140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu  
   145                  150                  155                  160

Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln  
                   165                  170                  175

Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met  
                   180                  185                  190

Ala



## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ACG TGC GGT TCC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 13	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCG CAT GGC GTC AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATA AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCT TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCA	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAT CAC ATC ACT AAT GAC	240
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GAG CAT CAC ATC TTG CAT	298
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His	
85 90 95	
CTT CCA GGA TGC GTC CCC TGT GTG AGA ACT GGG AAC CAG TCA CGA TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG ATA GCC TTG ACC CCT ACG TTG GCC GCG CCA CAC ATT GGC GCT CCA	384
Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro	



115	120	125	
CTT GAG TCC ATG CGA CGT CAT GTG GAT TTG ATG GTA GGC ACT GCC ACA			432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr			
130	135	140	
TTG TGC TCC GCA CTC TAC ATT GGA GAT CTG TGC GGA GGC ATA TTT CTA			480
Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu			
145	150	155	160
GTG GGC CAG ATG TTC AAC TTC AGG CCC CGC CTG CAC TGG ACC ACC CAG			528
Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln			
165	170	175	
GAG TGC AAT TGT TCC ATC TAT CCA GGC CAC ATC ACG GGT CAC AGA ATG			576
Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met			
180	185	190	
GCG			579
Ala			

## (2) INFORMATION FOR SEQ ID NO: 174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val			
20	25	30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser			
50	55	60	
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp			
65	70	75	80
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His			
85	90	95	
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys			
100	105	110	
Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro			
115	120	125	



Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln  
 165 170 175  
 Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu-Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC	240
Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp	



65	70	75	80	
TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT				288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His				
85		90	95	
CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC				336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys				
100	105		110	
TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG				384
Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro				
115	120		125	
CTC GAA TCC ATG CCG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC				432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr				
130	135		140	
GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG				480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu				
145	150	155	160	
GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CGC CAT TGG ACT ACC CAG				528
Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln				
165	170		175	
GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA ATG				576
Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met				
180	185		190	
GCT				579
Ala				

## (2) INFORMATION FOR SEQ ID NO: 176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60



Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80

Cys Pr Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
 '85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys  
 100 105 110

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro  
 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met  
 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ACG TGC GGG TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCT 48  
 Thr Cys Gly Phe Ala Asp Leu Met-Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15

CCA GTA GGA GGC GTC GCC AGA GCC TTG GCG CAT GGC GTC AGG GCT GTG 96  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val



227

20	25	30	
GAG GAC GGG ATC AAT TAC GCA ACA GGG AAC CTT CCC GGC TGC TCC TTT Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45			144
TCT ATC TTC CTC TTG GTA CTT CTC TCG CGC CTA ACT GTC CCA GCG TCT Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser 50 55 60			192
GCT CAG CAC TAC CGG AAT GCA TCG GGC ATC TAC CAT GTC ACC AAC GAC Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80			240
TGC CCG AAC TCC AGT ATT GTG TAT GAA GCC GAC CAT CAC ATC ATG CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85 90 95			288
CTA CCC GGG TGT GTG CCC TGT GTA AGA ACT GGG AAT GTC TCG CGT TGC Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys 100 105 110			336
TGG ATT CCT TTA ACA CCC ACT GTA GCC GTC CCC TAC CTC GGG GCT CCA Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro 115 120 125			384
CTT ACG TCT GTA CGG CAG CAT GTG GAC CTG ATG GTG GGG GCG GCC ACC Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140			432
TTA TGC TCT GCC CTC TAC ATC GGA GAC CAT TGC GGA GGT GTC TTC TTG Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu 145 150 155 160			480
GCA GGG CAG ATG GTC AGT TTC CAA CCC CGG CGT CAT TGG ACT ACC CAG Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175			528
GAT TGC AAC TGT TCC ATC TAT GTG GGC CAC ATC ACC GGC CAC AGG ATG Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met 180 185 190			576
GCC Ala			579

## (2) INFORMATION FOR SEQ ID NO: 178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

SUBSTITUTE SHEET (RULE 26)



Thr Cys Gly Phe Ala Asp Leu M t Gly Tyr Ile Pro L u Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro  
 115 120 125  
 Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu  
 145 150 155 160  
 Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

ACCTGCGGCT TCGCCGACCT CATGGGATAC ATCCCGCTCG TAGGCGCCCC CGTGGGAGGC      60
GTCCGCAGAR CTCTGGCGCA TGGCTCAGG GCTCTGAAG ACGGGATCAA TTATGCAACA      120
GGGAATCTTC CTGGTTGCTC TTCTCTATC TCGCTTCTTG AACTTCTCTC GTGCCTGACT      180
GTTCCCGCCT CAGCCATCCA CTATCGCAAT GCTTCGGACG GTTATTATAT CACCAATGAT      240
TGCCCGAACT CTAGCATAGT GTATGAAGCC GAGAACCACA TCTTGACACT TCCGGGGTGT      300
ATACCCTGTG TGAAGACCGG GAATCAGTCG CGGTGCTGGG TGGCTCTCAC CCCCACGCTG      360
GCGGCCCCAC ACCTACGTGC TCCGCTTCG TCGTTACGGG CGCATGTGGA CCTAATGGTG      420
GGGGCCGCCA CGGCATGCTC CGCTTTTAC ATTGGAGATC TGTGCGGGGG TGTGTTTTTG      480
GCGGGCCAAC TGTTCACTAT CCGGCCACGC ATTCATGAAA CCACTCAGGA CTGCAATTGC      540
TCCATCTACT CAGGGCACAT CACGGGTNNN NNNNNNNN      579

```

## (2) INFORMATION FOR SEQ ID NO: 180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1           5           10           15

Pro Val Gly Gly Val Ala Arg Xaa Leu Ala His Gly Val Arg Ala Leu
                20           25           30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35           40           45

Ser Ile Ser Leu Leu Glu Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50           55           60

Ala Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile Thr Asn Asp
65           70           75           80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Glu Asn His Ile Leu His
85           90           95

Leu Pro Gly Cys Ile Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys
100          105          110

```



Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro His Leu Arg Ala Pro  
 115 120 125  
 Leu S r Ser Leu Arg Ala His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Ala Cys Ser Ala Phe Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160  
 Ala Gly Gln Leu Phe Thr Ile Arg Pro Arg Ile His Glu Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly Xaa Xaa Xaa  
 180 185 190  
 Xaa

## (2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..578

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

GCGTGCGGCT TCGCCGATCT CATGGGATAC ATCCCGCTCG TAGGCGCCCC CGTGGGTGGC	60
GTCCGCCAGAG CCCTGGCGCA CGGTGTTAGG GCTGTGGAGG ACGGGATTAA CTACGCAACA	120
GGGAATCTTC CTGGTTGCTC TTTCTCTATC TNCCTTCTGG CACTTCTCTC GTGCCTGACT	180
GTCCCGGCCT CGGCTCAGCA CTACCGGAAT GTCTCGGGCA TCTACCACGT CACCAATGAT	240
TGCCCCGAATT CCAGCATAGT GTATGAAGCC GATCACCACA TCATGCACTT ACCAGGGTGC	300
ATACCCTGCG TGAGGACCGG GAACGTTTCG CGCTGCTGGG TATCTCTGAC ACCTACTGTG	360
GCTGCTCCCT ACCTCGGGGC TCCGCTTACG TCGCTACGGC GGCATGTGGA TTTGATGGTG	420
GGTGCAAGCA CCCTTTGCTC TGCCCTCTAC GTCGGAGACC TCTGTGGAGG TGTCTTCTTA	480



GTGGGACAGA TGTTCACCTT CCAGCCGCGC CGCCACTGGA CCACTCAGGA CTGCAACTGC 540  
TCCATTACG TCGGCCACAT CACAGGCCAC AGAATGGCT 579

## (2) INFORMATION FOR SEQ ID NO: 182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
1 5 10 15  
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
20 25 30  
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
35 40 45  
Ser Ile Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
50 55 60  
Ala Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp  
65 70 75 80  
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
85 90 95  
Leu Pro Gly Cys Ile Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys  
100 105 110  
Trp Val Ser Leu Thr Pro Thr Val Ala Ala Pro Tyr Leu Gly Ala Pro  
115 120 125  
Leu Thr Ser Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
130 135 140  
Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160  
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
165 170 175  
Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met  
180 185 190  
Ala



## (2) INFORMATION FOR SEQ ID NO: 183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

ACC TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTA GAA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGT ATT AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TCC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCA	192
Ser Ile Ser Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC GTC AAC TAT CGC AAC GCC TCG GGC GTC TAT CAT ATC ACC AAT GAC	240
Ala Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT TCG AGC ATA GTG TAC GAG GCT GAC TAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Tyr His Ile Leu His	
85 90 95	
CTC CCT GGG TGC TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTT ACT CCC ACC GTG GCG GCG CCT TAC GTT GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro	



115	120	125	
CTA GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCT GCT ACT			432
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr			
130	135	140	
GTG TGC TCC GCT CTT TAC ATC GGG GAC CTG TGC GGT GGC GTA TTT TTG			480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu			
145	150	155	160
GTT GGT CAG ATG TTT TCT TTC CAG CCG CGA CCG CAC TGG ACC ACG CAG			528
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln			
165	170	175	
GAC TGC AAT TGT TCT ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG			576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met			
180	185	190	
GCA			- 579
Ala			

## (2) INFORMATION FOR SEQ ID NO: 184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala
1				5					10					15	
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val
			20					25					30		
Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe
	35						40					45			
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Thr	Ser
	50					55				60					
Ala	Val	Asn	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp
	65				70				75					80	
Cys	Pro	Asn	Ala	Ser	Ile	Val	Tyr	Glu	Thr	Glu	Asn	His	Ile	Leu	His
		85						90					95		
Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Thr	Gly	Asn	Gln	Ser	Arg	Cys
		100						105					110		
Trp	Val	Ala	Leu	Thr	Pro	Thr	Val	Ala	Ser	Pro	Tyr	Ala	Gly	Ala	Pro
	115					120					125				
Leu	Glu	Pro	Leu	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr
	130					135					140				

SUBSTITUTE SHEET (RULE 26)



Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Glu Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Ser Phe Trp His Phe Ser Arg Ala • Leu Ser Arg Pro Arg  
 50 55 60  
 Leu Ser Thr Thr Gly Met Ser Arg Ala Ser Thr Thr Ser Pro Met Ile  
 65 70 75 80  
 Ala Arg Ile Pro Ala • Cys Met Lys Pro Ile Thr Thr Ser Cys Thr  
 85 90 95  
 Tyr Gln Gly Ala Tyr Pro Ala • Gly Pro Gly Thr Phe Arg Ala Ala  
 100 105 110  
 Gly Tyr Leu • His Leu Leu Trp Leu Leu Pro Thr Ser Gly Leu Arg  
 115 120 125  
 Leu Arg Arg Tyr Gly Gly Met Trp Ile • Trp Trp Val Gln Pro Pro  
 130 135 140  
 Phe Ala Leu Pro Ser Thr Ser Glu Thr Ser Val Glu Val Ser Ser •  
 145 150 155 160  
 Trp Asp Arg Cys Ser Pro Ser Ser Arg Ala Ala Thr Gly Pro Leu Arg  
 165 170 175  
 Thr Ala Thr Ala Pro Phe Thr Ser Ala Thr Ser Gln Ala Thr Glu Trp

SUBSTITUTE SHEET (RULE 26)



## (2) INFORMATION FOR SEQ ID NO: 185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC	240
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His	
85 90 95	
CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA	384



Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro	
115 120 125	
GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT	432
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr	
130 135 140	
GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GGA TTC TTG	480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	
145 150 155 160	
GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG	528
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met	
180 185 190	
GCA	579
Ala	

## (2) INFORMATION FOR SEQ ID NO: 186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp	
65 70 75 80	
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His	
85 90 95	
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro	
115 120 125	

SUBSTITUTE SHEET (RULE 26)



Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr  
 130 135 140

Val Cys S r Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met  
 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC	240



Ala Val Asn Tyr Arg Asn Ala Ser Gly Il	Tyr His Ile Thr Asn Asp	
65	70	75
		80
TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC		288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Il Leu His		
85	90	95
CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CCG TGC		336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys		
100	105	110
TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG		384
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro		
115	120	125
CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT		432
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr		
130	135	140
GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TCC GGT GGC GTA TTT TTG		480
Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu		
145	150	155
		160
GTT GGT CAG ATG TTC TCT TTC CAG CCG CCG CAC TGG ACT ACG CAG		528
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln		
165	170	175
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG		576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met		
180	185	190
GCA		
Ala		579

## (2) INFORMATION FOR SEQ ID NO: 188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1	5
	10
	15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20	25
	30
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35	40
	45
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50	55
	60



Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
65 70 75 80

Cys Pro Asn Ser Ser Il Val Tyr Glu Thr Glu His His Ile Leu His  
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr  
130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met  
180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC  
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
1 5 10 15

48



CCC GTT GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30	96
GAG GAC GGG ATT AAC TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45	144
TCT ATC TTC CTC CTG GCA CTT CTT TCG TGC CTC ACT GTC CCA GCG TCA Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60	192
GCT GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC AAT GAC Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80	240
TGT CCG AAT TCC AGC GTA GTC TAT GAA ACT GAC CAC CAT ATA TTG CAC Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His 85 90 95	288
TTG CCG GGG TGC GTA CCC TGC GTG AGG GCC GGG AAC GTG TCT CGT TGC Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys 100 105 110	336
TGG ACG CCG GTA ACA CCT ACG GTG GCT GCC GTA TCC ATG GAC GCT CCG Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro 115 120 125	384
CTC GAG TCC TTC CGG CGG CAT GTG GAC CTA ATG GTA GGT GCG GCC ACC Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140	432
GTG TGT TCT GTC CTC TAT GTT GGA GAC CTC TGT GGA GGT GCT TTC CTA Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160	480
GTG GGG CAG ATG TTC ACC TTC CAG CCG CTT CGC CAC TGG ACC ACG CAG Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175	528
GAT TGT AAT TGC TCC ATC TAT ACT GGC CAT ATC ACC GGC CAC AGG ATG Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met 180 185 190	576
GCG Ala	579

## (2) INFORMATION FOR SEQ ID NO: 190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro  
 115 120 125  
 Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS



(B) LOCATION: 1..289

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..286

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACT AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT	96
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT AGG AAG ACT TCG GAG CCG TCG CAA CCT CTT GGG AGA CGT CAG CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	
65 70 75 80	
TAC CCA TGG CCT CTT TAC GGT AAT GAG GGT TGT GGG TGG GCA GGA TGG G	289
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	

## (2) INFORMATION FOR SEQ ID NO: 192:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	



65		70		75		80									
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp
				85					90					95	

## (2) INFORMATION FOR SEQ ID NO: 193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..498

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..495

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCT ATG GAC GTA AAG TTC CCG GGC GGT GGA CAG ATC GTT GGC	96
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGC AGG CGT CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCG CGC CGG TCC GAG GGC AGG TCC TGG GCG CAA GCC GGG	240
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly	
65 70 75 80	
TAC CCC TGG CCC CTC TAT GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCT CCT CGC GGC TCT CGG CCA TCT TGG GGC CCA AAT GAT CCC	336



Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro  
 100 105 110  
 CGG CGG AGA TCG CGC AAT CTG GGT AAG GTC ATC GAT ACC CTG ACG TGC 384  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC CCC GTC 432  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val  
 130 135 140  
 GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG GAG GAC 480  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
 145 150 155 160  
 GGG ATT AAC TAT CGA CAG 498  
 Gly Ile Asn Tyr Arg Gln  
 165

## (2) INFORMATION FOR SEQ ID NO: 194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val  
 130 135 140

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Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
145 150 155 160

Gly Ile Asn Tyr Arg Gln  
165

## (2) INFORMATION FOR SEQ ID NO: 195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC	144
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT	240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	
85 90 95	
GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC	336

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246

Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Lys	Asp	Asn	Val	Ser	Arg	Cys		
			100					105					110				
TGG	GTC	CAA	ATT	ACC	CCC	ACG	CTG	TCA	GCC	CCG	AGC	TTC	GGA	GCA	GTC	384	
Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Phe	Gly	Ala	Val		
			115				120					125					
ACG	GCT	CCC	CTT	CGG	AGA	GCC	GTT	GAT	TAC	TTG	GTG	GGA	GGG	GCT	GCC	432	
Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Val	Gly	Gly	Ala	Ala		
			130				135				140						
CTC	TGC	TCC	GCG	TTA	TAC	GTT	GGA	GAC	GCG	TGT	GGG	GCA	CTA	TTT	TTG	480	
Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	Gly	Ala	Leu	Phe	Leu		
			145			150				155				160			
GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	CGC	CAG	CAT	GCT	ACG	GTG	CAG	528	
Val	Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	Gln	His	Ala	Thr	Val	Gln		
			165				170				175						
GAC	TGC	AAC	TGT	TCC	ATC	TAC	AGT	GGC	CAC	GTC	ACC	GGC	CAT	CAG	ATG	576	
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	His	Val	Thr	Gly	His	Gln	Met		
			180				185					190					
GCA																579	
Ala																	

## (2) INFORMATION FOR SEQ ID NO: 196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Gly
1				5					10					15	
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu
			20				25						30		
Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe
	35					40					45				
Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser
	50					55					60				
Ala	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp
	65				70				75					80	
Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Leu	Ile	Leu	His
			85					90					95		
Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Lys	Asp	Asn	Val	Ser	Arg	Cys
			100					105						110	

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Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val  
 115 120 125  
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG	192

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Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC	240
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His	
85 90 95	
CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA	384
Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro	
115 120 125	
GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT	432
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr	
130 135 140	
GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GTA TTC TTG	480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	
145 150 155 160	
GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG	528
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met	
180 185 190	
GCA	579
Ala	

## (2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	

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35	40	45
Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser		
50	55	60
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp		
65	70	75 80
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His		
85	90	95
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys		
100	105	110
Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro		
115	120	125
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr		
130	135	140
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu		
145	150	155 160
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln		
165	170	175
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met		
180	185	190
Ala		

## (2) INFORMATION FOR SEQ ID NO: 199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1470

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..1467

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:



A TCA CCA CCG GAG CTT CTA TCA CAT ACT CCA CTT ACG GCA AGT TCC Ser Pro Pro Glu Leu Leu Ser His Thr Pro Leu Thr Ala Ser Ser 1 5 10 15	46
TTG CTG ATG GAG GGT GTT CAG GCG GCG CGC ATG ACG TGA TCA TAT GCG Leu Leu Met Glu Gly Val Gln Ala Ala Arg Met Thr * Ser Tyr Ala 20 25 30	94
ACG AGT GCC ATT CCC AGG ACG CCA CCA CCA TTC TTG GGA TAG GCA CTG Thr Ser Ala Ile Pro Arg Thr Pro Pro Pro Phe Leu Gly * Ala Leu 35 40 45	142
TCC TTG ACC AGG CAG AGA CCG CTG GAG CTA GGC TCG TCG TCT TGG CCA Ser Leu Thr Arg Gln Arg Arg Leu Glu Leu Gly Ser Ser Ser Trp Pro 50 55 60	190
CGG CCA CCC CTC CCG GCA GTG TGA CAA CGC CCC ACC CCA ACA TCG AGG Arg Pro Pro Leu Pro Ala Val * Gln Arg Pro Thr Pro Thr Ser Arg 65 70 75	238
AAG TGG CCC TGC CTC AGG AGG GGG AGG TTC CCT TCT ACG GCA GAG CCA Lys Trp Pro Cys Leu Arg Arg Gly Arg Phe Pro Ser Thr Ala Glu Pro 80 85 90 95	286
TTC CCC TTG CTT TTA TAA AGG GTG GTA GGC ATC TCA TCT TCT GCC ATT Phe Pro Leu Leu Leu * Arg Val Val Gly Ile Ser Ser Ser Ala Ile 100 105 110	334
CCA AGA AAA AAT GTG ATG AAC TCG CCA AGC AAC TGA CCA GCC TGG GCG Pro Arg Lys Asn Val Met Asn Ser Pro Ser Asn * Pro Ala Trp Ala 115 120 125	382
TGA ACG CCG TGG CAT ATT ATA GAG GTC TAG ACG TCG CCG TCA TAC CCA * Thr Pro Trp His Ile Ile Glu Val * Thr Ser Pro Ser Tyr Pro 130 135 140	430
CAA CAG GAG ACG TGG TCG TGT GCA GCA CCG ACG CGC TCA TGA CCG GAT Gln Gln Glu Thr Trp Ser Cys Ala Ala Pro Thr Arg Ser * Arg Asp 145 150 155	478
TCA CCG GCG ACT TTG ATT CTG TCA TAG ACT GCA ACT CCG CCG TCA CTC Ser Pro Ala Thr Leu Ile Leu Ser * Thr Ala Thr Pro Pro Ser Leu 160 165 170 175	526
AGA CGG TGG ACT TCA GTC TGG ATC CCA CTT TTA CCA TTG AGA CTA CCA Arg Arg Trp Thr Ser Val Trp Ile Pro Leu Leu Pro Leu Arg Leu Pro 180 185 190	574
CAG TGC CCC AGG ACG CAG TGT CCA GAA GCC AGC GTT GGG GCC GCA CCG Gln Cys Pro Arg Thr Gln Cys Pro Glu Ala Ser Val Gly Ala Ala Arg 195 200 205	622
GGA GAG GTA GGC ACG GCA TAT ACC GGT ATG TCT CGG CTG GAG AGA GAC Gly Glu Val Gly Thr Ala Tyr Thr Gly Met Ser Arg Leu Glu Arg Asp 210 215 220	670
CGT CTG GCA TGT TCG ACT CCG TGG TGC TCT GTG AGT GCT ACG ATG CCG Arg Leu Ala Cys Ser Thr Pro Trp Cys Ser Val Ser Ala Thr Met Pro 225 230 235 240 245	718

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225	230	235	
GAT GTG CAT GGT ACG ATC TGA CTC CTG CCG AGA CTA CCG TGA GGT TGC Asp Val His Gly Thr Ile * Leu Leu Pro Arg Leu Pro * Gly Cys 240 245 250 255			766
GCG CTT ACT AAA CAC CCC CGG GCT CCC TGT CTG TCA GGA CCA TTT GGA Ala Leu Thr Lys His Pro Arg Ala Pro Cys Leu Ser Gly Pro Phe Gly 260 265 270			814
ATT CTG GGA GGG GGT GTT CAC GGG GCT CAC TAA CAT CGA CGC TCA CAT Ile Leu Gly Gly Gly Val His Gly Ala His * His Arg Arg Ser His 275 280 285			862
GCT GTC ACA GAC CAA ACA GGG TGG GGA GAA TTT CCC ATA CCT TGT AGC Ala Val Thr Asp Gln Thr Gly Trp Gly Glu Phe Pro Ile Pro Cys Ser 290 295 300			910
GTA CCA AGC AAC AGT CTG TGT TCG CGC GAA AGC GCC CCC CCC CAG CTG Val Pro Ser Asn Ser Leu Cys Ser Arg Glu Ser Ala Pro Pro Gln Leu 305 310 315			958
GGA CAC AAT GTG GAA ATG CAT GCT CCG TCT CAA ACC GAC TTA ACT GGC Gly His Asn Val Glu Met His Ala Pro Ser Gln Thr Asp Leu Thr Gly 320 325 330 335			1006
CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC ACA Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile Thr 340 345 350			1054
CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG GAC Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp 355 360 365			1102
TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG GCG Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val Ala 370 375 380			1150
GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC GGT Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val Gly 385 390 395			1198
AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG GTA Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val 400 405 410 415			1246
TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG CCC Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu Pro 420 425 430			1294
TAT ATG GAC GAA ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA GTG Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys Val 435 440 445			1342
CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG CCG Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys Pro 450 455 460			1390



GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG CCA CAT ACA 1438  
 Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Pro His Thr  
 465 470 475

TGT GGA ACT TCA TCA GTG GGA TAC AAT AAT AG 1470  
 Cys Gly Thr Ser Ser Val Gly Tyr Asn Asn  
 480 485

## (2) INFORMATION FOR SEQ ID NO: 197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TGTGCCAGGA CCATCACCAC CGGAGCTTCT ATCACA TACT CCAC TTACGG CAAGTTCCTT 60  
 GCTGATGGAG GGTGTT CAGG CGGCGCGCAT GACGTGATCA TATGCGACGA GTGCCATTCC 120  
 CAGGACGCCA CCACCAT TCT TGGGATAGGC ACTGTCCTTG ACCAGGCAGA GACGGCTGGA 180  
 GCTAGGCTCG TCGTCTTGGC CACGGCCACC CCTCCCGGCA GTGTGACAAC GCCCCACCCC 240  
 AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTT CTTTCTACGG CAGAGCCATT 300  
 CCCCTTGCTT TTATAAAGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAATGT 360  
 GATGAACTCG CCAAGCAACT GACCAGCCTG GCGGTGAACG CCGTGGCATA TTATAGAGGT 420  
 CTAGACGTCG CCGTCATACC CACAACAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC 480  
 ATGACGGGAT TCACCGGCGA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG 540  
 ACGGTGGACT TCAGTCTGGA TCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC 600  
 GCAGTGTCCA GAAGCCAGCG TTGGGGCCGC ACGGGGAGAG GTAGGCACGG CATATACCGG 660  
 TATGTCTCGG CTGGAGAGAG ACCGTCTGGC ATGTTGCACT CCGTGGTGCT CTGTGAGTGC 720  
 TACGATGCCG GATGTGCATG GTACGATCTG ACTCCTGCCG AGACTACCGT GAGGTTGCGC 780  
 GCTTACNTAA ACACCCCCGG GCTCCCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG 840  
 GTGTTACCGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG 900  
 GAGAATTTCC CATACCTTGT AGCGTACCAA GCAACAGTCT GTGTTGCGCG GAAAGCGCCC 960



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CCCCCAGCT GGGACACAAT GTGGAATGC ATGCTCCGTC TCAAACCGAC NTTAACTGGC      1020
CCTACTCCCC TCTTGACAG GCTGGGGCCC GTCCAGAATG AGATCACACT GACGCACCCC      1080
ATCACCAAGT ACATTATGGC TTGCATGTCT GCGGACTTGG AGGTCAATTAC CAGCACTTGG      1140
GTTCTGGTGG GGGGCGTTGT GGGGGCCCTG GCGGCTTACT GCTTGACGGT GGGTTCGGTA      1200
GCCATAGTCG GTAGGATCAT CCTCTCTGGG AAACCTGCCA TCATTCCCGA TAGGGAGGTA      1260
TTATACCAGC AATTGATGA GATGGAGGAG TGCTCGGCTT CGTTGCCCTA TATGGACGAA      1320
ACACGTGCCA TTGCCGGACA ATTCAAAGAG AAAGTGCTCG GCTTCATCAG CACGACCGGC      1380
CAGAAGGCTG AAACCTTGAA GCCGGCAGCC ACGTCTGTGT GGAACAAGGC TGAGCAGTTC      1440
TGGNCCACAT ACATGTGGAA CTTTCATCAGT GGGATACAAT AATAG                      1485

```

## (2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr
1           5           10           15
Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val
20          25          30
Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly
35          40          45
Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val
50          55          60
Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro
65          70          75          80
Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr
85          90          95
Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile
100         105         110
Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr
115         120         125
Ser Leu Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala
130         135         140

```

SUBSTITUTE SHEET (RULE 26)



Val Ile Pro Thr Thr Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu  
 145 150 155 160  
 Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser  
 165 170 175  
 Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile  
 180 185 190  
 Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Trp  
 195 200 205  
 Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala  
 210 215 220  
 Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Val Val Leu Cys Glu Cys  
 225 230 235 240  
 Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr  
 245 250 255  
 Val Arg Leu Arg Ala Tyr Xaa Asn Thr Pro Gly Leu Pro Val Cys Gln  
 260 265 270  
 Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile  
 275 280 285  
 Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro  
 290 295 300  
 Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro  
 305 310 315 320  
 Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro  
 325 330 335  
 Xaa Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln  
 340 345 350  
 Asn Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys  
 355 360 365  
 Met Ser Ala Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly  
 370 375 380  
 Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val  
 385 390 395 400  
 Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro  
 405 410 415  
 Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser  
 420 425 430  
 Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe  
 435 440 445



Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu  
450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe  
465 470 475 480

Trp Xaa Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TGTGCCAGGA CCATCACCAC CGGAGCTTCT ATCACAFACT CCACTTACGG CAAGTTCCCT	60
GCTGATGGAG GGTGTTGAGG CGGCGCGTAT GACGTGATCA TATGCCACGA GTGCCATTCC	120
CAGGACGCCA CCACCAATTCT TGGGATAGGC ACTGTCCCTG ACCAGGCAGA GACGGCTGGA	180
GCTAGGCTCG TCGTCTTGGC CACGGCCACT CTTCCCGGCA GTGTGACAAC GCCCCACCCC	240
AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTT CTTCTACGG CAGAGCCATT	300
CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAATGT	360
GATGAACTCG CCAAGCAACT GACCAGCCTG GGGGTGAACG CCGTGGCATA TTATAGAGGT	420
CTAGACGTCG CCGTCATCCC CACAGCAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC	480
ATGACGGGAT TCACCGGCGA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG	540
ACGGTGGACT TCAGTCTGGA TCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC	600
GCAGTGTCCA GAAGCCAGCG TAGGGGCGGC ACGGGGAGAG GTAGGCACGG CATATACCGG	660
TATGTCTCGG CTGGAGAGAG ACCNTCTGAC ATGTTGACT CCGTGGTGCT CTGTGAGTGC	720
TACGATGCCG GATGTGCGTG GTATGATCTG ACTCTGCGG AGACTACCGT GAGGTTGCGC	780
GCTTACATAA ACACCCCGG GTCCTCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG	840
GTGTTACCGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG	900
GAGAATTTC CATACTTGT AGCGTACCAA GCAACAGTCT GTGTTGCGGC GAAAGCGCCC	960



```

CCCCCAGCT GGGACACAAT GTGGAAATGC ATGCTCCGTC TCAAACCGAC TTAACTGGC      1020
CCTACTCCCC TCTTGACAG GCTGGGGCCC GTCCAGANTG AGATCACACT GACGCACCCC      1080
ATCACCAAGT ACATTATGGC TTGCATGTCT GCGGACTTGG AGGTCATTAC CANCACTTGG      1140
GTTCTGGTGG GGGGCGTTGT GCGGGCCCTG GCGGCTTACT GCTTGACGGT GGGTTCGGTA      1200
GCCATAGTCG GTAGGATCAT CCTCTCTGGG AAACCTGCCA TCATTCCCGA TAGGGAGGCA      1260
TTATACCAGC AATTGTATGA GATGGAGGAG TGCTGGGCTT CTTTGCCCTA TATGGACGAG      1320
ACACGTGCCA TTGCCGGACA ATTCAAAGAG AAAGTGCTCG GCTTCATCAG CACGACCGGC      1380
CAGAAGGCTG AAACCTCTGAA GCCGGCAGCC ACCTCTGTGT GGAACAAGGC TGAGCAGTTC      1440
TGGGCCACAT ACATGTGGAA CTTTCATCAGC GGGATACAAT AATAG                      1485

```

## (2) INFORMATION FOR SEQ ID NO: 200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr
1           5           10           15
Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val
20          25          30
Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly
35          40          45
Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val
50          55          60
Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro
65          70          75          80
Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr
85          90          95
Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile
100         105         110
Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr
115         120         125

```



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Ser Leu Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala  
 130 135 140

Val Ile Pro Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu  
 145 150 155 160

Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser  
 165 170 175

Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile  
 180 185 190

Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg  
 195 200 205

Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala  
 210 215 220

Gly Glu Arg Xaa Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys  
 225 230 235 240

Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr  
 245 250 255

Val Arg Leu Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln  
 260 265 270

Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile  
 275 280 285

Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Xaa Pro  
 290 295 300

Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro  
 305 310 315 320

Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro  
 325 330 335

Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln  
 340 345 350

Xaa Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys  
 355 360 365

Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val Leu Val Gly  
 370 375 380

Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val  
 385 390 395 400

Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro  
 405 410 415

Asp Arg Glu Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser  
 420 425 430

Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe

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435

440

445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu  
 450 455 460

Thr Leu Lys Pr Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe  
 465 470 475 480

Trp Ala Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

C TCC ACT GTG ACT GAG AGA GAC ATC AGG GTC GAA GAA GAA GTC TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA ACC GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu	
20 25 30	
ACG GAG AGA CTC TAC GTG GGC GGC CCT ATG TAC AAT AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	
CTT TGC GGG TAT CGC AGG TGC CGC GCA AGC GGC GTA TAT ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAC CTT AAA GCC TCA GCA GCC ATC AGG	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCT GCG GGG CTG AAG GAC TGC ACC ATG CTG GTT TGC GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	



GTC GTG ATC GCT GAA AGC GGT GGC GTC GAG GAG GAC AAG CGA GCC CTC 334  
 Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu  
                   100                  105                  110

GGA GCT 340  
 Gly Ala

## (2) INFORMATION FOR SEQ ID NO: 202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln  
   1                  5                  10                  15  
 Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr  
                   20                  25                  30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu  
                   35                  40                  45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
                   50                  55                  60  
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala  
                   65                  70                  75                  80  
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                   85                  90                  95  
 Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly  
                   100                  105                  110

Ala

## (2) INFORMATION FOR SEQ ID NO: 203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO



## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 2..340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 2..337

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

C TCC ACA GTG ACT GAA AGA GAC ATC AGG GTC GAG GAA GAG GTC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCT GAA ACC CGC AAG GTA ATA TCT GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACT GAA AGA CTC TAT GTG GGC GGT CCC ATG CAC AAC AGC AGG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp	
35 40 45	
CTA TGC GGG TAC CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACA AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACT CTG ACG TGC TTC CTC AAG GCC ACA GCG GCC ACC AAA	238
Phe Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys	
65 70 75	
GCC GCT GGC CTA AAG GAC TGC ACC ATG TTG GTG TGT GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTT ATC GCC GAA AGC GAT GGT GTC GAA GAG GAC CGC CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu	
100 105 110	
GGA GCT	
Gly Ala	340

## (2) INFORMATION FOR SEQ ID NO: 204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15



Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu Thr  
           20                                  25                                  30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu  
           35                                  40                                  45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
           50                                  55                                  60  
 Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys Ala  
           65                                  70                                  75                                  80  
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                                   85                                  90                                  95  
 Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu Gly  
           100                                  105                                  110  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..337

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

C TCC ACG GTG ACC GAA AGG GAT ATC AGG ACC GAG GAA GAG ATC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr	
1                                  5                                  10                                  15	
CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu	
20                                  25                                  30	
ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35                                  40                                  45	



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[illegible]

(2) INFORMATION FOR SEQ ID NO: 206:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln  
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr  
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu  
35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
50 55 60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala  
65 70 75 80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg  
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 207:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

C TCC ACG GTG ACT GAA AGG GAC ATT AGG GTC GAG GAA GAG ATC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Ile Tyr	
1 5 10 15	
CAG TGC TGT GAC CTG GAG CCC GAG GCA CGC AAG GTG ATA TCC GCT CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACA GAA AGA CTC TAC AAG GGC GGC CCC ATG TAT AAC AGC AAG GGG GAC	142
Thr Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	
CTA TGC GGG CTT CGG AGG TGC CGC GCA AGC GGG GTA TAC ACC ACA AGC	190
Leu Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACG GTG ACA TGC TAC CTT AAA GCC ACA GCA GCC ACC AGG	238
Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg	
65 70 75	
GCT GCA GGG CTG AAA GAT TGC ACT ATG CTG GTA TGC GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTT ATT GCC GAA AGC GGT GGC GTG GAG GAG GAC GCC CGA GCC CTC	334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 208:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
 1             5             10             15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr
      20             25             30

Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
      35             40             45

Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
      50             55             60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
      65             70             75             80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
      85             90             95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
      100             105             110

Ala

```

## (2) INFORMATION FOR SEQ ID NO: 209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..340

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

CCCCACCGTG ACNGAGAGGG ACNTCAGGGT CGAGGAAGAG GTCTATCAGT GCTGTAATCT      60
GGAGNCCGAT GNCCGCAAGG TCATCAACGC CCTCACAGAG AGACTCTACG TGGGCGGGCC      120

```



TATGCACAAC AGCAAGGGAG ACCTGTGTGG CATCGTAGA TGCCGCGCGA GCGGCGTTA 180  
 CACCACGAGC TTCGGAACA CGCTGACTTG CTACCTCAA GCCACAGCGG CCACCAGGGC 240  
 CGCGGGCTTG AAGGATTGCA CCATGCTGGT CTGCGGAGAC GACCTGGTTG TCATTGCTGA 300  
 GAGCATTGGC ATAGACGAGG ACAAGCAAGC CCTCTGACT 340

## (2) INFORMATION FOR SEQ ID NO: 210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Pro Thr Val Thr Glu Arg Asp Xaa Arg Val Glu Glu Glu Val Tyr Gln  
 1 5 10 15  
 Cys Cys Asn Leu Glu Xaa Asp Xaa Arg Lys Val Ile Asn Ala Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu  
 35 40 45  
 Cys Gly Ile Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
 50 55 60  
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala  
 65 70 75 80  
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ala Glu Ser Ile Gly Ile Asp Glu Asp Lys Gln Ala Leu Arg  
 100 105 110  
 Thr

## (2) INFORMATION FOR SEQ ID NO: 211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA



(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```

CTCSACTGTG NCCGAGAGGG ACATCAGGAC AGAGGGAGAG GTCTATCAGT GTTGCGACCT      60
GGAACCGGAA GCCCGCAAGG TAATCACCGC CCTCACTGAG AGACTCTATG TGGGCGGACC      120
CATGTTCAAC AGCAAGGGAG ACCTGTGCGG ACAACGCCGG TGCCGCGCAA GCGGCGTGTT      180
CACCACCAGC TTCGGGAACA CACTGACGTG CTACCTTAAA GCCACAGCTG CTACTAGAGC      240
AGCCGGCTTA AAAGATTGCA CCATGCTGGT CTGCGGTGAC GACTTAGTGG TTATTTCGGA      300
GAGCGCCGGT GTGGAGGAGG ATCCCAAAAC CCNCGACCN                               340

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

Ser Thr Val Xaa Glu Arg Asp Ile Arg Thr Glu Gly Glu Val Tyr Gln
1           5           10           15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
          20           25           30
Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu
          35           40           45
Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Phe
          50           55           60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala

```

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Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu  
 80 85 90 95

GTC GTT ATC TGT GAA AGC GCG GGA ACC CAA GAG GAC GCG GCG AGC CTA 334  
 Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu  
 100 105 110

CGA GTC  
 Arg Val 340

## (2) INFORMATION FOR SEQ ID NO: 214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln  
 1 5 10 15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu Thr  
 20 25 30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn  
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys  
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg Ala  
 65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95

Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg  
 100 105 110

Val

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

C TCA ACC GTC ACG GAG AGG GAT ATA AGA ACA GAA GAA TCC ATA TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CAA GCT TGT TCC CTG CCC CAA GAG GCC AGA ACT GTC ATA CAC TCG CTC	94
Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu	
20 25 30	
ACC GAG AGA CTC TAC GTG GGA GGG CCC ATG ATA AAC AGC AAA GGG CAA	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln	
35 40 45	
TCC TGC GGT TAC AGG CGT TGC CGC GCA AGC GGT GTT TTC ACC ACC AGC	190
Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGG AAT ACC ATG ACG TGT TAC ATC AAA GCC CTT GCA GCG TGT AAA	238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys	
65 70 75	
GCC GCA GGG ATC GTG GAC CCC GTC ATG CTG GTG TGT GGA GAC GAC CTG	286
Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATC TCG GAG AGC CAG GGT AAC GAG GAG GAC GAG CGA AAC CTG	334
Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu	
100 105 110	
AGA GCT	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln  
 1 5 10 15  
 Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met  
 50 55 60  
 Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala  
 65 70 75 80  
 Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu Arg  
 100 105 110  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..340

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

C TCG ACT GTC ACT GAA CAG GAC ATC AGG GTG GAA GAG GAG ATA TAT 46  
 Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Ile Tyr  
 1 5 10 15  
 CAA TGC TGC AAC CTT GAA CCG GAG GCC AGC AAA GTG ATC TCC TCC CTC 94  
 Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu



20	25	30	
ACG GAG CGG CTT TAC TGC GGA GGC CCT ATG TTT AAC AGC AAG GGG GCC			142
Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala			
35	40	45	
CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC AGC			190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser			
50	55	60	
TTT GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA ACG GCC GCG AAG			238
Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys			
65	70	75	
GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT CTG			286
Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu			
80	85	90	95
GTC GTG GTG GCT GAG AGT GAT GGC GTC GAC GAG GAT AGA GCA GCC CTG			334
Val Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu			
100	105	110	
AGA GCC			340
Arg Ala			

## (2) INFORMATION FOR SEQ ID NO: 218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln			
1	5	10	15
Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu Thr			
20	25	30	
Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln			
35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe			
50	55	60	
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys Ala			
65	70	75	80
Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	
Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu Arg			
100	105	110	



Ala

## (2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Arg Thr Glu Gly Arg Thr Ser Trp Ala Gln  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 629 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 3..629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC	47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala	
1 5 10 15	
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG	95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu	
20 25 30	
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA	143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
35 40 45	
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CCG CTT AAG CCA ACA CTA	191
Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu	
50 55 60	
CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA	239
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu	
65 70 75	
ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA	287
Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser	
80 85 90 95	
GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG CTT GGA GGG GTC	335
Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val	
100 105 110	
CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT TGT GTT GTG ATT	383
Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile	
115 120 125	
GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC GTT CCA GAC AAA	431
Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys	
130 135 140	



GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG TGC TCA CAA GCT 479  
 Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala  
 145 150 155

GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC CAG TTC AAG GAA 527  
 Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu  
 160 165 170 175

AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA CAA GCT GTC ATT 575  
 Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile  
 180 185 190

GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG GCC TTT TGG CAC 623  
 Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His  
 195 200 205

AAG CAT 629  
 Lys His

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His  
 1 5 10 15

Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr  
 20 25 30

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser  
 35 40 45

Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His  
 50 55 60

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile  
 65 70 75 80

Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala  
 85 90 95

Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val Leu  
 100 105 110

Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile Val  
 115 120 125

Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu  
 130 135 140



Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala Ala  
 145 150 155 160

Pr Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu Lys  
 165 170 175

Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile Glu  
 180 185 190

Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His Lys  
 195 200 205

His

## (2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 2..12

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Ile His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Val Asn Tyr His Asn Thr Ser Gly Ile Tyr His Leu  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Leu Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Val Trp Gln Leu Arg Ala Ile Val Leu His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 233:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Val Tyr Glu Ala Asp Tyr His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Val Tyr Glu Thr Asp Asn His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Val Phe Glu Thr Val His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Val Phe Glu Thr Glu His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Val Phe Glu Thr Asp His His Ile Met His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu  
1 5 10



## (2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Val Tyr Glu Ala Asp Ala Leu Ile Leu His Ala  
1                    5                    10

## (2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Val Gln Asp Gly Asn Thr Ser Ala Cys Trp Thr Pro Val  
1                    5                    10

## (2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1                    5                    10

## (2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu



1

5

10

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Val Lys Thr Gly Asn Ser Val Arg Cys Trp Ile Pro Leu  
1                    5                    10

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Val Lys Thr Gly Asn Val Ser Arg Cys Trp Ile Ser Leu  
1                    5                    10

## (2) INFORMATION FOR SEQ ID NO: 249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Val Arg Lys Asp Asn Val Ser Arg Cys Trp Val Gln Ile  
1                    5                    10

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ala Pro Ser Phe Gly Ala Val Thr Ala Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:



Ala Pro Tyr Ile Gly Ala Pro Val Glu Ser  
1                      5                      10

1

**S**

**10**

- (2) INFORMATION FOR SEQ ID NO: 254:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(A) LENGTH: 10 amino acids

(8) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Ala Gln His Leu Asn Ala Pro Leu Glu Ser  
1 5 10

1

5

10

- (2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Ser Pro Tyr Val Gly Ala Pro Leu Glu Pro  
1 5 10

1

5

10

- (2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Ser Pro Tyr Ala Gly Ala Pro Leu Glu Pro  
1 5 10

1

5

10

- (2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids

(A) LENGTH: 10 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asn Val Pro Tyr Leu Gly Ala Pr Leu Thr Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Pro His Leu Arg Ala Pro Leu Ser Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Ala Pro Tyr Leu Gly Ala Pro Leu Thr Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Pro Arg Gln His Ala Thr Val Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 264:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Ser	Pro	Gln	His	His	Lys	Phe	Val	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Arg	Pro	Arg	Arg	Leu	Trp	Thr	Thr	Gln	Glu
1				5					10

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Pro	Pro	Arg	Ile	His	Glu	Thr	Thr	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Thr Ile Ser Tyr Ala Asn Gly Ser Gly Pro Ser Asp Asp Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ser Arg Arg Gln Pro Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser  
1 5 10 15

Trp Ala Gln

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1443

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ACC ATC ACC ACC GGA GCT TCT ATC ACA TAC TCC ACT TAC GGC AAG TTC  
Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe

48



1	5	10	15	
CTT GCT GAT GGA GGG TGT TCA GGC GGC GCG TAT GAC GTG ATC ATA TGC				96
Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys				
20		25	30	
GAC GAG TGC CAT TCC CAG GAC GCC ACC ACC ATT CTT GGG ATA GGC ACT				144
Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr				
35	40		45	
GTC CTT GAC CAG GCA GAG ACG GCT GGA GCT AGG CTC GTC GTC TTG GCC				192
Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala				
50	55		60	
ACG GCC ACC CCT CCC GGC AGT GTG ACA ACG CCC CAC CCC AAC ATC GAG				240
Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu				
65	70	75	80	
GAA GTG GCC CTG CCT CAG GAG GGG GAG GTT CCC TTC TAC GGC AGA GCC				288
Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala				
85	90		95	
ATT CCC CTT GCT TTT ATA AAG GGT GGT AGG CAT CTC ATC TTC TGC CAT				336
Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His				
100	105		110	
TCC AAG AAA AAA TGT GAT GAA CTC GCC AAG CAA CTG ACC AGC CTG GGC				384
Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly				
115	120		125	
GTG AAC GCC GTG GCA TAT TAT AGA GGT CTA GAC GTC GCC GTC ATC CCC				432
Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro				
130	135		140	
ACA GCA GGA GAC GTG GTC GTG TGC AGC ACC GAC GCG CTC ATG ACG GGA				480
Thr Ala Gly Asp Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly				
145	150	155	160	
TTC ACC GGC GAC TTT GAT TCT GTC ATA GAC TGC AAC TCC GCC GTC ACT				528
Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr				
165	170		175	
CAG ACG GTG GAC TTC AGT CTG GAT CCC ACT TTT ACC ATT GAG ACT ACC				576
Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr				
180	185		190	
ACA GTG CCC CAG GAC GCA GTG TCC AGA AGC CAG CGT AGG GGC CGC ACG				624
Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr				
195	200		205	
GGG AGA GGT AGG CAC GGC ATA TAC CGG TAT GTC TCG GCT GGA GAG AGA				672
Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg				
210	215	220		
CCG TCT GAC ATG TTC GAC TCC GTG GTG CTC TGT GAG TGC TAC GAT GCC				720
Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala				
225	230	235	240	



290

GGA TGT GCG TGG TAT GAT CTG ACT CCT GCC GAG ACT ACC GTG AGG TTG Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu 245 250 255	768
CGC GCT TAC ATA AAC ACC CCC GGG CTC CCT GTC TGT CAG GAC CAT TTG Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 260 265 270	816
GAA TTC TGG GAG GGG GTG TTC ACG GGG CTC ACT AAC ATC GAC GCT CAC Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His 275 280 285	864
ATG CTG TCA CAG ACC AAA CAG GGT GGG GAG AAT TTC CCA TAC CTT GTA Met Leu Ser Gln Thr Lys Gln Gly Gly Gln Asn Phe Pro Tyr Leu Val 290 295 300	912
GCG TAC CAA GCA ACA GTC TGT GTT CGC GCG AAA GCG CCC CCC CCC AGC Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser 305 310 315 320	960
TGG GAC ACA ATG TGG AAA TGC ATG CTC CGT CTC AAA CCG ACT TTA ACT Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr 325 330 335	1008
GGC CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 340 345 350	1056
ACA CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 355 360 365	1104
GAC TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val 370 375 380	1152
GCG GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val 385 390 395 400	1200
GGT AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu 405 410 415	1248
GCA TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu 420 425 430	1296
CCC TAT ATG GAC GAG ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys 435 440 445	1344
GTG CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys 450 455 460	1392
CCG GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG GCC ACA Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr 465 470 475 480	1440

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TAC  
Tyr

1443

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```

Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe
 1           5           10           15
Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys
          20           25           30
Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr
          35           40           45
Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala
          50           55           60
Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu
          65           70           75           80
Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala
          85           90           95
Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His
          100          105          110
Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly
          115          120          125
Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro
          130          135          140
Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly
          145          150          155          160
Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr
          165          170          175
Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr
          180          185          190
Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr
          195          200          205
Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg
          210          215          220
Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala

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225	230	235	240
Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu			
245	250	255	
Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu			
260	265	270	
Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His			
275	280	285	
Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro Tyr Leu Val			
290	295	300	
Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser			
305	310	315	320
Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr			
325	330	335	
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile			
340	345	350	
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala			
355	360	365	
Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val			
370	375	380	
Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val			
385	390	395	400
Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu			
405	410	415	
Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu			
420	425	430	
Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys			
435	440	445	
Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys			
450	455	460	
Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr			
465	470	475	480
Tyr			